

## AMENDMENT

### In the Specification:

Please insert a new paragraph on page 1, beginning at line 4, immediately before the heading "BACKGROUND OF THE INVENTION", as follows:

#### **--SUBMISSION ON COMPACT DISC**

The content of the following submission on compact discs is incorporated herein by reference in its entirety: A compact disc copy of the Sequence Listing (CRF) (file name: 514572002000, date recorded: June 9, 2006, size: 184,320 bytes); a duplicate compact disc copy of the Sequence Listing (COPY 1) (file name: 514572002000, date recorded: June 9, 2006, size: 184,320 bytes); and a duplicate compact disc copy of the Sequence Listing (COPY 2) (file name: 514572002000, date recorded: June 9, 2006, size: 184,320 bytes). --

Please replace Table 1, beginning on page 6, with a new Table 1 as follows:

Table 1. Exemplary Influenza A Virus Primers

Id	Sequence	SEQ ID NO:
PMIA_00001	TTTGTGCGACAATGCTTCA	<u>1</u>
PMIA_00002	GACATTTGAGAAAGCTTGCC	<u>2</u>
PMIA_00003	AGGGACAACCTNGAACCTGG	<u>3</u>
PMIA_00004	AGGAGTTGAACCAAGACGCATT	<u>4</u>
PMIA_00005	ACCACATTCCCTTATACTGGAG	<u>5</u>
PMIA_00006	TTAGTCATCATCTTTCTCACAACA	<u>6</u>
PMIA_00007	ACAAATTGCTTCAAATGAGAAC	<u>7</u>
PMIA_00008	TGTCTCCGAAGAAATAAGATCC	<u>8</u>
PMIA_00009	GCGCAGAGACTTGAAGATGT	<u>9</u>
PMIA_00010	CCTTCCGTAGAAGGCCCT	<u>10</u>

Please replace Table 2, beginning on page 6 and bridging to page 7, with a new Table 2 as follows:

Table 2. Exemplary Influenza B Virus Primers

Id	Sequence	SEQ ID NO:
PMIB_00001	CACAATGGCAGAATTTAGTGA	<u>11</u>
PMIB_00002	GTCAGTTTGATCCCGTAGTG	<u>12</u>
PMIB_00003	CAGATCCCAGAGTGGACTCA	<u>13</u>
PMIB_00004	TGTATTACCCAAGGGTTGTTAC	<u>14</u>
PMIB_00005	GATCAGCATGACAGTAACAGGA	<u>15</u>
PMIB_00006	ATGTTCTGGTAAAAGTCGTTTAT	<u>16</u>
PMIB_00007	CCACAGGGGAGATTCCAAAG	<u>17</u>
PMIB_00008	GACATTCTTCCTGATTCATAATC	<u>18</u>
PMIB_00009	CAAACAACGGTAGACCAATATA	<u>19</u>
PMIB_00010	AGGTCAGTATCTATCACAGTCTT	<u>20</u>
PMIB_00011	ATGTCCAACATGGATATTGAC	<u>21</u>
PMIB_00012	GCTCTTCCTATAAATCGAATG	<u>22</u>
PMIB_00013	TGATCAAGTGATCGGAAGTAG	<u>23</u>
PMIB_00014	GATGGTCTGCTTAATTGGAA	<u>24</u>
PMIB_00015	ACAGAAGATGGAGAAGGCAA	<u>25</u>
PMIB_00016	ATTGTTTCTTTGGCCTGGAT	<u>26</u>

Please replace Table 3, beginning on page 7, with a new Table 3 as follows:

Table 3. Exemplary Human Metapneumovirus Primers

Id	Sequence	SEQ ID NO:
PMM_00001	CATCCCCAAAAATTGCCAGAT	<u>27</u>
PMM_00002	TTTGGGCTTTGCCTTAAATG	<u>28</u>
PMM_00003	ACACCCTCATCATTGCAACA	<u>29</u>
PMM_00004	GCCCTTCTGACTGTGGTCTC	<u>30</u>

Id	Sequence	SEQ ID NO:
PMM_00005	CGACACAGCAGCAGGAATTA	<u>31</u>
PMM_00006	TCAAAGCTGCTTGACACTGG	<u>32</u>
PMM_00007	CAAGTGCGACATTGATGACC	<u>33</u>
PMM_00008	TAATTCCTGCTGCTGTGTCG	<u>34</u>
PMM_00009	GCGACTGTAGCACTTGACGA	<u>35</u>
PMM_000010	TCATGATCAGTCCCGCATAA	<u>36</u>
PMM_000011	TGTTTCAGGCCAATACACCA	<u>37</u>
PMM_000012	TCATGATCAGTCCCGCATAA	<u>38</u>
PMM_000013	TCATGGGTAATGAAGCAGCA	<u>39</u>
PMM_000014	GGAGTTTTCCTCATCTGGA	<u>40</u>
PMM_000015	TCCAGTGATGGGAAACTCC	<u>41</u>
PMM_000016	TGTTGAGCTCCTTTGCCTTT	<u>42</u>

Please replace Table 4, beginning on page 7 and bridging to page 9, with a new Table 4 as follows:

Table 4. Exemplary Human Adenovirus Primers

Id	Sequence	SEQ ID NO:
PMAd1_00001	TGGCGGTATAGGGTAACTG	<u>43</u>
PMAd1_00002	ATTGCGGTGATGGTTAAAGG	<u>44</u>
PMAd1_00003	TTTTGCCGATCCCACTTATC	<u>45</u>
PMAd1_00004	GCAAGTCTACCACGGCATT	<u>46</u>
PMAd2_00001	CTCCGTTATCGCTCCATGTT	<u>47</u>
PMAd2_00002	AAGGACTGGTCGTTGGTGTC	<u>48</u>
PMAd2_00003	AAATGCCGTGGTAGATTTGC	<u>49</u>
PMAd2_00004	GTTGAAGGGGTTGACGTTGT	<u>50</u>
PMAd3_00001	TCCTCTGGATGGCATAGGAC	<u>51</u>

<u>Id</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
PMAd3_00002	TGTTGGTGTTAGTGGGCAA	<u>52</u>
PMAd3_00003	ACATGGTCCTGCAAAGTTCC	<u>53</u>
PMAd3_00004	GCATTGTGCCACGTTGTATC	<u>54</u>
PMAd4_00001	CGCTTCGGAGTACCTCAGTC	<u>55</u>
PMAd4_00002	CTGCATCATTGGTGTCAACC	<u>56</u>
PMAd4_00003	GGCACCTTTTACCTCAACCA	<u>57</u>
PMAd4_00004	TCTGGACCAAGAACCAGTCC	<u>58</u>
PMAd5_00001	GGCCTACCCTGCTAACTTCC	<u>59</u>
PMAd5_00002	ATAAAGAAGGGTGGGCTCGT	<u>60</u>
PMAd5_00003	ATCGCAGTTGAATGCTGTTG	<u>61</u>
PMAd5_00004	GTTGAAGGGGTTGACGTTGT	<u>62</u>
PMAd7_00001	ACATGGTCCTGCAAAGTTCC	<u>63</u>
PMAd7_00002	GATCGAACCCTGATCCAAGA	<u>64</u>
PMAd7_00003	AACACCAACCGAAGGAGATG	<u>65</u>
PMAd7_00004	CCTATGCCATCCAGAGGAAA	<u>66</u>
PMAd11_00001	CAGATGCTCGCCAAC TACAA	<u>67</u>
PMAd11_00002	AGCCATGTAACCCACAAAGC	<u>68</u>
PMAd11_00003	ACGGACGTTATGTGCCTTTC	<u>69</u>
PMAd11_00004	GGAATATTGGTTGCATTGG	<u>70</u>
PMAd21_00001	ACTGGTTCCTGGTCCAGATG	<u>71</u>
PMAd21_00002	AGCCATGTAACCCACAAAGC	<u>72</u>
PMAd21_00003	CTGGATATGGCCAGCACTTT	<u>73</u>
PMAd21_00004	CACCTGAGGTTCTGGTTGGT	<u>74</u>

<u>Id</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
PMAd23_00001	TAATGAAAAGGGCGGACAAG	<u>75</u>
PMAd23_00002	GCCAATGTAGTTTGGCCTGT	<u>76</u>
PMAd23_00003	AACTCCGCGGTAGACAGCTA	<u>77</u>
PMAd23_00004	CGTAGGTGTTGGTGTGGTG	<u>78</u>

Please replace Table 5, beginning on page 9, with a new Table 5 as follows:

Table 5. Exemplary HCoV-OC229E Primers

<u>Id</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
PMV_a0053	TCACTTGCTTCCGTTGAGGTTGGGCTGGCGGTTTAGAGTTGA	<u>79</u>
PMV_a0054	GGTTTCGGATGTTACAGCGTGTCGACCGCCCTTGTTTATGG	<u>80</u>
PMV_a0055	TCACTTGCTTCCGTTGAGGGCGTTGTTGGCCTTTTTCTTGTCT	<u>81</u>
PMV_a0056	GGTTTCGGATGTTACAGCGTGCCCGGCATTATTTTCATTGTTCTG	<u>82</u>
PMV_a0057	TCACTTGCTTCCGTTGAGGACAAAAGCCGCTGGTGGTAAAG	<u>83</u>
PMV_a0058	GGTTTCGGATGTTACAGCGTCAGAAATCATAACGGGCAAACCTCA	<u>84</u>
PMV_a0059	TCACTTGCTTCCGTTGAGGAAGAGTTATTGCTGGCGTTGTTGG	<u>85</u>
PMV_a0060	GGTTTCGGATGTTACAGCGTGCCCGGCATTATTTTCATTGTTCTG	<u>86</u>
PMV_b0053	TTGGGCTGGCGGTTTAGAGTTGA	<u>87</u>
PMV_b0054	GTGCGACCGCCCTTGTTTATGG	<u>88</u>
PMV_b0055	GCGTTGTTGGCCTTTTTCTTGTCT	<u>89</u>
PMV_b0056	GCCCGGCATTATTTTCATTGTTCTG	<u>90</u>
PMV_b0057	ACAAAAGCCGCTGGTGGTAAAG	<u>91</u>
PMV_b0058	CAGAAATCATAACGGGCAAACCTCA	<u>92</u>
PMV_b0059	AAGAGTTATTGCTGGCGTTGTTGG	<u>93</u>
PMV_b0060	GCCCGGCATTATTTTCATTGTTCTG	<u>94</u>

Please replace Table 6, beginning on page 9 and bridging to page 10, with a new Table 6 as follows:

Table 6. Exemplary HCoV-OC43 Primers

Id	Sequence	SEQ ID NO:
PMV_a0061	TCACTTGCTTCCGTTGAGGTTGGGGTGATGGGTTTCAGATTA A	<u>95</u>
PMV_a0062	GGTTTCGGATGTTACAGCGTCTCGGGAAGATCGCCTTCTTCTA	<u>96</u>
PMV_b006 1	TTGGGGTGATGGGTTTCAGATTAA	<u>97</u>
PMV_b006 2	CTCGGGAAGATCGCCTTCTTCTA	<u>98</u>

Please replace Table 7, beginning on page 10 and bridging to page 11, with a new Table 7 as follows:

Table 7. Exemplary Influenza A Virus Probes

Id	Sequence	SEQ ID NO:
PBIA_00001	TTTAGAGCCTATGTGGATGGATTCTRAACCGAACGGCTGCATTGAGGGCAAGCT TTCTCAAATGTC	<u>99</u>
PBIA_00002	ACAATTGAAGAAAGATTTGAAATCACTGGAACCATGCGCAGGCTTGCCGACCA AAGTCTCCCACCGAACT	<u>100</u>
PBIA_00003	AGCAATNGAGGAGTGCCTGATTAANGATCCCTGGGTTTTGCTNAATGC	<u>101</u>
PBIA_00004	CCATACAGCCATGGAACAGGAACAGGATACACCATGGACACAGTCAACAGAAC ACANCAATATTCAGAAA	<u>102</u>
PBIA_00005	GGGCGGGGAGTCTTCGAGCTCTCNGACGAAAAGGCAACGAACCCGATCGTGCC	<u>103</u>
PBIA_00006	GATCTNGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTACCTCT GACTAA	<u>104</u>

Please replace Table 8, beginning on page 11, with a new Table 8 as follows:

Table 8. Exemplary Influenza B Virus Probes

Id	Sequence	SEQ ID NO:
PBIB_00001	GCTGGGAAATAGCATGGAAGTATGATATTCAGCTACAATCAAGACTATTCGT TAAGTAATGAATCCTCA	<u>105</u>
PBIB_00002	TCTGTTCCAGCTGGTTTCTCCAATTTTGAAGGAATGAGGAGCTACATAGACAA TATAGATCCTAAAGGAG	<u>106</u>
PBIB_00003	TTACAACCATGAGCTACCAGAAGTTCCATATAATGCC'TTTCTTCTAATGTCTG ATGAATTGGGGCTGGCC	<u>107</u>
PBIB_00004	ACAAATAAGATCCAAATGAAATGGGGAATGGAAGCTAGAAGATGTCTGCTTCA ATCAATGCAACAAATGG	<u>108</u>
PBIB_00005	GAGGGAATGTATTCTGGAATAGANGAATGTATTAGTAACAACCCTTGGGTAAT ACAGAGTGCATACTGGT	<u>109</u>
PBIB_00006	CTACCGTGTTGGGAGTAGCCGCACTAGGTATCAAAAACATTGGAAACAAAGAA TACTTATGGGATGGACT	<u>110</u>
PBIB_00007	GGCTATGACTGAAAGAATAACCAGAGACAGCCCAATTTGGTTCCGGGATTTTT GTAGTATAGCACCGGTC	<u>111</u>
PBIB_00008	ACTGATCAGAGGAACATGATTCTTGAGGAACAATGCTACGCTAAGTGTGCAA CCTTTTGTAGGCCTGTT	<u>112</u>
PBIB_00009	AAAATCCCTTTGTNGGACATTTGTCTATTGAGGGCATCAAAGANGCAGATATA ACCCAGCACATGGTCC	<u>113</u>
PBIB_00010	CTTGGAATACAAGGGAATACAACCTTAAAACAAATGCTGAAGACATAGGAACCA AAGGCCAAATGTGCTCA	<u>114</u>
PBIB_00011	GTGGCAGGAGCAACATCAGCTGAGTTCATAGAAATGCTACACTGCTTACAAGG TGAAAATTGGAGACAAA	<u>115</u>
PBIB_00012	GGAACCCATCCCCGAAAGAGCAACCACAAGCAGTGAAGCTGATGTGCGGAAGG AAAACCCAAAAGAAACA	<u>116</u>
PBIB_00013	CTGTTTCCAAAGATCAAAGGCACTAAAAAGAGTTGGACTTGACCCTTCATTAA TCAGTACCTTTGCAGGA	<u>117</u>
PBIB_00014	AGAGTTTTGTCTGCATTAAACAGGCACAGAATTCAAGCCTAGATCAGCATTAAA ATGCAAGGGTTTCCATG	<u>118</u>
PBIB_00015	GAGGGACGTGATGCAGATGTCAAAGGAAATCTACTCAAGATGATGAATGACTC AATGGCTAAGAAAACCA	<u>119</u>
PBIB_00016	CCTATCAGGAATGGGAACAACAGCAACAAAAAGAAAGGCCTGATTCTAGCTG AGAGAAAAATGAGAAGA	<u>120</u>
PBIB_00017	GCAAGTCAAAGAATGGGGAAGGAATTGCAAAGGATGTAATGGAAGTGCTAAA GCAGAGCTCTATGGGAA	<u>121</u>

Please replace Table 9, beginning on page 11 and bridging to page 12, with a new Table 9 as follows:

Table 9. Exemplary Human Metapneumovirus Probes

Id	Sequence	SEQ ID NO:
PBM_00001	AAAAGTGTATCACAGAAGTTTGTTCATTGAGTATGGCAAAGCATTAGGCTCAT CATCTACAGGCAGCAAA	<u>122</u>
PBM_00002	GAAAGTCTATTTGTTAATATATTCATGCAAGCTTATGGAGCCGGTCAAACAAT GCTAAGGTGGGGGGTCA	<u>123</u>
PBM_00003	ACGCTGTTGTGTGGAGAAATCTGTATGCTAAACATGCTGATTACAAATATGC TGCAGAAATAGGAATAC	<u>124</u>
PBM_00004	TTAAGGAATCATCAGGTAATATCCCACAAAATCAGAGGCCCTCAGCACCAGAC ACACCCATAATCTTATT	<u>125</u>
PBM_00005	TGAGCAATCAAAGGAGTGCAACATCAACATATCCACTACAAATTACCCATGCA AAGTCAGCACAGGAAGA	<u>126</u>
PBM_00006	CTGTTCCATTGGCAGCAACAGAGTAGGGATCATCAAGCAGCTGAACAAAGGTT GCTCCTATATAACCAAC	<u>127</u>
PBM_00007	ACTTAATGACAGATGCTGAACTAGCCAGGGCCGTTTCTAACATGCCGACATCT GCAGGACAAATAAAATT	<u>128</u>
PBM_00008	AAAAAAGGGAAACTATGCTTGCCCTCTTAAGAGAAGACCAAGGGTGGTATTGT CAGAATGCAGGGTCAAC	<u>129</u>
PBM_00009	GAAAAGAACACACCAGTTACAATACCAGCATTTATCAAATCGGTTTCTATCAA AGAGAGTGAATCAGCCA	<u>130</u>
PBM_00010	CAAATCAGTTGGCAAAAAACACATGATCTGATCGCATTATGTGATTTTATGG ATCTAGAAAAGAACACA	<u>131</u>
PBM_00011	CAGCTAAAGACACTGACTATACTACTCTGTATGCTGCATCACAAAGTGGTCC AATACTAAAAGTGAATG	<u>132</u>
PBM_00012	AAAAGAACACACCAGTTACAATACCAGCATTTATCAAATCGGTTTCTATCAA GAGAGTGAATCAGCCAC	<u>133</u>
PBM_00013	CTATTATAGGAGAAAAAGTGAACACTGTATCTGAAACATTGGAATTACCTACT ATCAGTAGACCCACCAA	<u>134</u>
PBM_00014	AAGTTAGCATGGACAGACAAAGGTGGGGCAATCAAACTGAAGCAAAGCAAAC AATCAAAGTTATGGATC	<u>135</u>
PBM_00015	CAGGAAAATACACAAAGTTGGAGAAAGATGCTCTAGACTTGCTTTCAGACAAT GAAGAAGAAGATGCAGA	<u>136</u>
PBM_00016	CTAATAGCAGACATAATAAAGAAGCCAAGGGAAAAGCAGCAGAAATGATGGA AGAAGAAATGAACCAGC	<u>137</u>



Please replace Table 10, beginning on page 12 and bridging to page 13, with a new Table 10 as follows:

Table 10. Exemplary Human Adenovirus Probes

Id	Sequence	SEQ ID NO:
PBA <sub>d</sub> _00001	CTGACACCTACCAAGGTATAAAATCAAACGGAAACGGTAATCCTCAAAACTGG ACCAAAAATGACGATTT	<u>138</u>
PBA <sub>d</sub> _00002	TCCTCTACTCCAACATTGCACTGTACCTGCCTGACAAGCTAAAATACACTCCT ACAAATGTGGAAATATC	<u>139</u>
PBA <sub>d</sub> _00003	GCTATCGGAGGCAGAGTACTAAAAAGACTACTCCCATGAAACCATGCTACGG ATCGTATGCCAGACCTA	<u>140</u>
PBA <sub>d</sub> _00004	AGTATTGTTTTGTACAGTGAGGATGTTAATATGGAAACTCCTGATACTCACAT TTCATACAAACCAAGCA	<u>141</u>
PBA <sub>d</sub> _00005	GGGAAACGATCTTAGAGTTGACGGGGCTAGCATTAAAGTTTGACAGCATTTGTC TTTACGCCACCTTCTTC	<u>142</u>
PBA <sub>d</sub> _00006	TTGCCATTAAAAACCTCCTCCTGCCAGGCTCATATACATATGAATGGAAC TTCAGGAAGGATGTTAA	<u>143</u>
PBA <sub>d</sub> _00007	TTGCAACACGTAATGAAATAGGAGTGGGTAACAACCTTTGCCATGGAAATTAAC CTAAATGCCAACCTATG	<u>144</u>
PBA <sub>d</sub> _00008	TTGGGGTAACTGACACCTATCAAGCTATTAAGGCTAATGGCAATGGCTCAGGC GATAATGGAGATATTAC	<u>145</u>
PBA <sub>d</sub> _00009	AGGTATCAAGGCATTAAAGTTAAAACCGATGACGCTAATGGATGGGAAAAAGA TGCTAATGTTGATACAG	<u>146</u>
PBA <sub>d</sub> _00010	GAGAAGTTTTTCTGTACTCCAATGTGGCTTTGTACCTTCCAGATGTTTACAAGT ACACGCCACCTAACATT	<u>147</u>
PBA <sub>d</sub> _00011	ATCAGTCATTTAACGACTACCTCTCTGCAGCTAACATGCTTTACCCCATTCCT GCCAATGCAACCAACAT	<u>148</u>
PBA <sub>d</sub> _00012	CTACTTCGTATATTCTGGATCTATTCCCTACCTGGATGGCACCTTTTACCTTA ACCACACTTTCAAGAAG	<u>149</u>
PBA <sub>d</sub> _00013	ACCTGCCAGTGGAAGGATGCTAACAGCAAAATGCATACCTTTGGGGTAGCTGC CATGCCAGGTGTTACTG	<u>150</u>
PBA <sub>d</sub> _00014	ATAGAAGCTGATGGGCTGCCATTATAGAATAGATTCAACTTCTGGAAGTGACAC AGTAATTTATGCTGATA	<u>151</u>
PBA <sub>d</sub> _00015	TTGAAATTAAGCGCACCGTGGACGGCGAGGGGTACAACGTGGCCCAGTGCAAC ATGACCAAGGACTGGTT	<u>152</u>
PBA <sub>d</sub> _00016	CGGCAACGACCGGCTCCTGACGCCCAACGAGTTTGAAATTAAGCGCACCGTGG ACGGCGAGGGGTACAAC	<u>153</u>
PBA <sub>d</sub> _00017	CTCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTC	<u>154</u>

<b>Id</b>	<b>Sequence</b>	<b>SEQ ID NO:</b>
	TCTACGCCAACTCCGCC	
PBA <sub>d</sub> _00018	GCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATTACCCA GAAAAAGTTTCTTTGCG	<u>155</u>
PBA <sub>d</sub> _00019	ACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAAACACCTACGACTACATG AACAAGCGAGTGGTGGC	<u>156</u>
PBA <sub>d</sub> _00020	AAGATGAACTTCCAAATTACTGCTTTCCACTGGGAGGTGTGATTAATACAGAG ACTCTTACCAAGGTAAA	<u>157</u>
PBA <sub>d</sub> _00021	AGCTAACATGCTTTACCCCATCCCTGCCAATGCAACCAACATTCCAATTTCCA TCCCATCTCGCAACTGG	<u>158</u>
PBA <sub>d</sub> _00022	TTCAACTCTTGAAGCCATGCTGCGCAACGATACCAATGATCAGTCATTCAACG ACTACCTCTCTGCAGCT	<u>159</u>
PBA <sub>d</sub> _00023	AGGCTGTGGACAGCTATGATCCCGATGTTTCGTATTATTGAAAATCATGGCGTC GAGGATGAACTGCCTAA	<u>160</u>
PBA <sub>d</sub> _00024	TGAAATTGTGCTTTACACGGAAAATGTCAATTTGGAACTCCAGACAGCCATG TGGTATACAAGCCAGGA	<u>161</u>
PBA <sub>d</sub> _00025	CATCGGCTATCAGGGCTTCTACATTCCAGAAGGATACAAAGATCGCATGTATT CATTTTTTCAGAAACTTC	<u>162</u>
PBA <sub>d</sub> _00026	GCTGCTTCTCCCAGGCTCCTACACTTATGAGTGGAACCTTTAGGAAGGATGTGA ACATGGTTCTACAGAGT	<u>163</u>
PBA <sub>d</sub> _00027	ATGACACCAATGATCAGTCATTCAACGACTACCTATCTGCAGCTAACATGCTC TACCCCATTCCTGCCAA	<u>164</u>
PBA <sub>d</sub> _00028	CTTGCCAACTACAACATTGGATACCAGGGCTTCTACGTTTCCTGAGGGTTACAA GGATCGCATGTACTCCT	<u>165</u>
PBA <sub>d</sub> _00029	GATCGCATGTACTCCTTCTTCAGAACTTCCAGCCCATGAGTAGACAGGTGGT TGATGAGATTAAC TACA	<u>166</u>
PBA <sub>d</sub> _00030	CCCCTAAGGGCGCTCCCAATACATCTCAGTGGATTGCTGAAGGCGTAAAAAAA GAAGATGGGGGATCTGA	<u>167</u>
PBA <sub>d</sub> _00031	AGAAAATGTAAATTTGGAACTCCAGATTCCCATGTTGTTTACAAAGCAGGAA CTTCAGACGAAAGCTCT	<u>168</u>
PBA <sub>d</sub> _00032	TGTGGCTACCAATACTGTTTACCAAGGTGTTAAGTTACAAACTGGTCAAAC TG ACAAATGGCAGAAAGAT	<u>169</u>
PBA <sub>d</sub> _00033	CCGAATTGGGAAGGGTAGCGTATTCGCCATGGAAATCAATCTCCAGGCCAAC C TGTGGAAGAGTTTCTG	<u>170</u>

<b>Id</b>	<b>Sequence</b>	<b>SEQ ID NO:</b>
PBAd_00034	TTGATGAGGTCAATTACAAAGACTTCAAGGCCGTCGCCATACCCTACCAACAC AACAACTCTGGCTTTGT	<u>171</u>
PBAd_00035	TGACGAAGAGGAAGAGAAAAATCTCACCCTTACACTTTTGGAATGCCCCAG TGAAAGCAGAAGGTGGT	<u>172</u>
PBAd_00036	AGAAGATTTTGACATTGACATGGCTTTCTTTGATTCCAACACTATTAACACAC CAGATGTTGTGCTGTAT	<u>173</u>

Please replace Table 11, beginning on page 13 and bridging to page 14, with a new Table 11 as follows:

Table 11. Exemplary HCoV-OC229E Probes

<b>Id</b>	<b>Sequence</b>	<b>SEQ ID NO:</b>
PBS10049	AATGGGGTTATGTTGGTTCCTCTCCACTAATCACCATGCAATTTGTAATGTTCA TAGAAATGAGCATGT	<u>174</u>
PBS10050	GTGTATGACTGCTTTGTGAAGAATGTGGATTGGTCAATTACCTACCCTATGATAG CTAATGAAAATGCCA	<u>175</u>
PBS10051	TTGCATCTTCTTTTGTGGTATGCCATCTTTTGTTCATATGAAACAGCAAGACA AGAGTATGAAAATGC	<u>176</u>
PBS10052	AAATGGTTTCCTCACCACAAATAATCAAACAATTGAAGAAGGCTATGAATGTTGCA AAAGCTGAGTTTGAC	<u>177</u>
PBS10053	CTGCTGCAGCTATGTACAAAGAAGCACGTGCTGTTAATAGAAAATCAAAAGTTGT TAGTGCCATGCATAG	<u>178</u>
PBS10054	ACGTTTGGACATGTCTAGTGTGACACTATCCTTAATATGGCACGTAATGGTGT GTCCCTCTTTCCGTT	<u>179</u>
PBS10055	CTGGTGGTAAAGTTTCATTTCTGATGACGTTGAAGTAAAGACATTGAACCTGT TTACAGAGTCAAGCT	<u>180</u>
PBS10056	TTTACAGAGTCAAGCTTTGCTTTGAGTTTGAAGATGAAAACTTGTTAGATGTTTG TGAAAAGGCAATTGG	<u>181</u>
PBS10057	GATGTTTGTGAAAAGGCAATTGGCAAGAAAATTAAACATGAAGGTGACTGGGATA GCTTTTGTAAGACTA	<u>182</u>
PBS10058	GCGTTGTTGGCCTTTTCTTGTCTAAGCATAGTGATTTTGGTCTTGGTGATCTTG TCGATTCTTATTTTG	<u>183</u>

<b>Id</b>	<b>Sequence</b>	<b><u>SEQ ID NO:</u></b>
PBS10059	AGCAAGACAAGAGTATGAAAATGCTGTTGCAAATGGTTCCTCACCACAAATAATC AAACAATTGAAGAAG	<u>184</u>
PBS10060	TTGAAGAAGGCTATGAATGTTGCAAAGCTGAGTTTGACAGGGAATCATCTGTTC AAAAGAAAATTAACA	<u>185</u>
PBS10061	CTGCTGCAGCTATGTACAAAGAAGCACGTGCTGTTAATAGAAAATCAAAAGTTGT TAGTGCCATGCATAG	<u>186</u>

Please replace Table 12, beginning on page 14, with a new Table 12 as follows:

Table 12. Exemplary HCoV-OC43 Probes

<b>Id</b>	<b>Sequence</b>	<b><u>SEQ ID NO:</u></b>
PBS10062	CTCACATCCTAGGAAGATGCATAGTTTTAGATGTTAAAGGTGTAGAAGAATTGCATGACGATTTAGTTA A	<u>187</u>
PBS10063	GGATTGGCCATTGCACCATAGCTCAACTCACGGATGCAGCACTGTCCATTAAGGAAAATGTTGATTTTA T	<u>188</u>
PBS10064	GCATGCAATTCAATTATAAAATCACCATCAACCCCTCATCACGGCTAGACTTGAAATAGTTAAGCTCG G	<u>189</u>
PBS10065	ATAGTTAGTCACTGGATGGGAATTCGTTTTGAATACACATCACCCACTGATAAGCTAGCTATGATTATG G	<u>190</u>

Please replace Table 13, beginning on page 23 and bridging to page 24, with a new Table 13 as follows:

Table 13. Exemplary SARS-CoV probes

<b>probe_id</b>	<b>Sequence 5'-3'</b>	<b><u>SEQ ID NO:</u></b>	<b>region</b>
PBS00001	TTACCCTAATATGTTTATCACCCGCGAAGAAGCTATT CGTCACGTTTCGTGCGTGGA	<u>191</u>	SARS-Cov Replicase 1B
PBS00002	CTGACAAGTATGTCCGCAATCTACAACACAGGCTCTA TGAGTGTCTCTATAGAAAT	<u>192</u>	SARS-Cov Replicase 1B
PBS00003	CATAACACTTGCTGTAAC'TTATCACACCGTTTCTACA GGTTAGCTAACGAGTGTGC	<u>193</u>	SARS-Cov Replicase 1B
PBS00004	TTACCCTAATATGTTTATCACCCGCGAAGAAGCTATT CGTCACGTTTCGTG	<u>194</u>	SARS-Cov Replicase 1B
PBS00009	GCGTTCTCTTAAAGCTCCTGCCGTAGTGTCAAGTATCA TCACCAGATGCTGTTACTACATATAATGGATAC	<u>195</u>	SARS-Cov Replicase 1A

probe_id	Sequence 5'-3'	SEQ ID NO:	region
PBS00010	CTTTGGCTGGCTCTTACAGAGATTGGTCCTATTTCAGG ACAGCGTACAGAGTTAGGTGTTGAATTTCTTAA	<u>196</u>	SARS-Cov Replicase 1A
PBS00011	CTACGTAGTGAAGCTTTCGAGTACTACCATACTCTTG ATGAGAGTTTTCTTGGTAGGTACATGTCTGCTT	<u>197</u>	SARS-Cov Replicase 1A
PBS00012	TGCCAATTGGTTATGTGACACATGGTTTTAATCTTGA AGAGGCTGCGCGCTGTATGCGTTCTCTTAAAGC	<u>198</u>	SARS-Cov Replicase 1A
PBS00013	TATAAAGTTACCAAGGGAAAGCCCGTAAAAGGTGCTT GGAACATTGGACAACAGAGATCAGTTTTTAACAC	<u>199</u>	SARS-Cov Replicase 1A
PBS00014	TGCTTCATTGATGTTGTTAACAAGGCACTCGAAATGT GCATTGATCAAGTCACTATCGCTGGCGCAAAG	<u>200</u>	SARS-Cov Replicase 1A
PBS00015	TGTCGACGCCATGGTTTATACTTCAGACCTGCTCACC AACAGTGTCAATTATTATGGCATATGTAAGTGGT	<u>201</u>	SARS-Cov Replicase 1A
PBS00016	TACTGTTGAAAAACTCAGGCCTATCTTTGAATGGATT GAGGCGAAACTTAGTGCAGGAGTTGAATTTCTC	<u>202</u>	SARS-Cov Replicase 1A
PBS00017	ACCTATTCTGTTGCTTGACCAAGCTCTTGTATCAGAC GTTGGAGATAGTACTGAAGTTTCC	<u>203</u>	SARS-Cov Replicase 1A
PBS00018	GCCTATTAATGTCATAGTTTTTGTATGGCAAGTCCAAA TGCGACGAGTCTGCTTCTAAGTCTGCTTCTGTG	<u>204</u>	SARS-Cov Replicase 1A
PBS00019	TGAGAGCTAACAACACTAAAGGTTCACTGCCTATTAA TGTCATAGTTTTTGTATGGCAAGTCCAAATGCGA	<u>205</u>	SARS-Cov Replicase 1A
PBS00020	ACTTGCATGATGTGCTATAAGCGCAATCGTGCCACAC GCGTTGAGTGTACAACATTGTTAATGGCATGA	<u>206</u>	SARS-Cov Replicase 1A
PBS00021	GGCGATGTAGTGGCTATTGACTATAGACACTATTTCAG CGAGTTTCAAGAAAGGTGCTAAATTACTGCATA	<u>207</u>	SARS-Cov Replicase 1A
PBS00022	TCAAACCAAACACTTGGTGTTTACGTTGTCTTTGGAG TACAAAGCCAGTAGATACTTCAAATTCATTGGA	<u>208</u>	SARS-Cov Replicase 1A
PBS00023	TAGTGCTGTTGGCAACATTTGCTACACACCTTCCAAA CTCATTGAGTATAGTGATTTTGCTAC	<u>209</u>	SARS-Cov Replicase 1A
PBS00024	TCATAGCTAACATCTTTACTCCTCTTGTGCAACCTGT GGGTGCTTTAGATGTGTCTGCTTCAGTAGTGGC	<u>210</u>	SARS-Cov Replicase 1A
PBS00025	GGTATTATTGCCATATTGGTGACTTGTGCTGCCTACT ACTTTATGAAATTCAGACGTGTTTTTGGTGAGT	<u>211</u>	SARS-Cov Replicase 1A
PBS00026	GTGATGTCAGAGAACTATGACCCATCTTCTACAGCA TGCTAATTTGGAATCTGCAAAGCGAGTTCTTAA	<u>212</u>	SARS-Cov Replicase 1A
PBS00027	AACCATCAAGCCTGTGTCGTATAAACTCGATGGAGTT ACTTACACAGAGATTGAACCAAATTTGGATGGG	<u>213</u>	SARS-Cov Replicase 1A

probe_id	Sequence 5'-3'	SEQ ID NO:	region
PBS00028	GTTTTCTACAAGGAAACATCTTACACTACAACCATCA AGCCTGTGTCGTATAAACTCGATGGAGTTACTT	<u>214</u>	SARS-Cov Replicase 1A
PBS00029	CCTTGAATGAGGATCTCCTTGAGATACTGAGTCGTGA ACGTGTTAACATTAACATTGTTGGCGATTTTCA	<u>215</u>	SARS-Cov Replicase 1A
PBS00031	GCCATGGTTTTATACTTCAGACCTGCTCACCAACAGTG TCATTATTATGGCATATGTAACCTGGTGGTCTTG	<u>216</u>	SARS-Cov Replicase 1A
PBS00032	CAACAGACTTCTCAGTGGTTGTCTAATCTTTGGGCA CTACTGTTGAAAACTCAGGCCTATCTTTGAAT	<u>217</u>	SARS-Cov Replicase 1A
PBS00033	TTCCCGTCAGGCAAAGTTGAAGGGTGCATGGTACAAG TAACCTGTGGAAC TACAAC	<u>218</u>	SARS-Cov Replicase 1A
PBS00034	GGTTCACCATCTGGTGT TTTATCAGTGTGCCATGAGAC CTAATCATAACCATTAAGG	<u>219</u>	SARS-Cov Replicase 1A
PBS00035	AGATCATGTTGACATATTGGGACCTCTTTCTGCTCAA ACAGGAATTGCCGTC	<u>220</u>	SARS-Cov Replicase 1A
PBS00036	TAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAG CCTTTGCCGCAGAGACAAAAGAAGCAGCCCACT	<u>221</u>	SARS-Cov Nucleocapsid gene
PBS00037	ACGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACTT CTATTACCTAGGAAC TGGCCCAGAAGCTTCACT	<u>222</u>	SARS-Cov Nucleocapsid gene
PBS00038	GGCGCTAACAAAAGAAGGCATCGTATGGGTTGCAACTG AGGGAGCCTTGAATACACCCAAAGACCACATTG	<u>223</u>	SARS-Cov Nucleocapsid gene
PBS00039	GTCCAGATGACCAAATTTGGCTACTACCGAAGAGCTAC CCGACGAGTTCTGTGGTGGTGACGGCAAAATGAA	<u>224</u>	SARS-Cov Nucleocapsid gene
PBS00040	GAGGTGGTGAAACTGCCCTCGCGCTATTGCTGCTAGA CAGATTGAACCAGCTTGAGAGCAAAGTTTCTGG	<u>225</u>	SARS-Cov Nucleocapsid gene
PBS00041	AAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCCGCA GAGACAAAAGAAGCAGCCCACTGTGACTCTTCT	<u>226</u>	SARS-Cov Nucleocapsid gene
PBS00042	AAATTGCACAATTTGCTCCAAGTGCCTCTGCATTCTT TGGAATGTCACGCATTGGCATGGAAGTCACACC	<u>227</u>	SARS-Cov Nucleocapsid gene
PBS00043	ACCAATTTAACAAGGCGATTAGTCAAATTTCAAGAATC ACTTACAACAACATCAACTGCATTGGGCAAGCT	<u>228</u>	SARS-Cov Spike glycoprotein gene
PBS00044	CACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCT ATATCAAGATGTTAACTGCACTGATGTTTCTAC	<u>229</u>	SARS-Cov Spike glycoprotein gene
PBS00045	AAAGGGCTACCACCTTATGTCCTTCCCACAAGCAGCC CCGCATGGTGTGTCTTCCTACATGTCACGTAT	<u>230</u>	SARS-Cov Spike glycoprotein gene

probe_id	Sequence 5'-3'	SEQ ID NO:	region
PBS00046	TCAGGAAATTGTGATGTCGTTATTGGCATCATTAAACA ACACAGTTTATGATCCTCTGCAACCTGAGCTTG	<u>231</u>	SARS-Cov Spike glycoprotein gene
PBS00047	TTGATCTTGGCGACATTTTCAGGCATTAACGCTTCTGT CGTCAACATTCAAAAAGAAATTGACCGCCTCAA	<u>232</u>	SARS-Cov Spike glycoprotein gene
PBS00048	GAGGAACTTCACCACAGCGCCAGCAATTTGTCATGAA GGCAAAGCATACTTCCCTCGTGAAGGTGTTTTT	<u>233</u>	SARS-Cov Spike glycoprotein gene

Please replace Table 15, beginning on page 28 and bridging to page 38, with a new Table 15 as follows:

Table 15. Exemplary probes for non-SARS-CoV infectious organisms causing SARS-like symptoms

seqid	sequence (5'-3')	SEQ ID NO:	species
PBIA_00001	TTTAGAGCCTATGTGGATGGATTTCRAACCGAACGGC TGCATTGAGGGCAAGCTTTCTCAAATGTC	<u>234</u>	Influenza A virus
PBIA_00002	ACAATTGAAGAAAGATTTGAAATCACTGGAACCATG CGCAGGCTTGCCGACCAAAGTCTCCACCGAACT	<u>235</u>	Influenza A virus
PBIA_00003	AGCAATNGAGGAGTGCCTGATTAANGATCCCTGGGT TTTGCTNAATGC	<u>236</u>	Influenza A virus
PBIA_00004	CCATACAGCCATGGAACAGGAACAGGATACACCATG GACACAGTCAACAGAACACANCAATATTCAGAAA	<u>237</u>	Influenza A virus
PBIA_00005	GGGCGGGGAGTCTTCGAGCTCTCNGACGAAAAGGCA ACGAACCCGATCGTGCC	<u>238</u>	Influenza A virus
PBIA_00006	GATCTNGAGGCTCTCATGGAATGGCTAAAGACAAGA CCAATCCTGTACCTCTGACTAA	<u>239</u>	Influenza A virus
PBIB_00001	GCTGGGAAATAGCATGGAATGATGATATTCAGCTA CAATCAAGACTATTTCGTTAAGTAATGAATCCTCA	<u>240</u>	Influenza B virus
PBIB_00002	TCTGTTCCAGCTGGTTTCTCCAATTTTGAAGGAATG AGGAGCTACATAGACAATATAGATCCTAAAGGAG	<u>241</u>	Influenza B virus
PBIB_00003	TTACAACCATGAGCTACCAGAAGTTCCATATAATGC CTTCTTCTAATGTCTGATGAATTGGGGCTGGCC	<u>242</u>	Influenza B virus
PBIB_00004	ACAAATAAGATCCAAATGAAATGGGGAATGGAAGCT AGAAGATGTCTGCTTCAATCAATGCAACAAATGG	<u>243</u>	Influenza B virus
PBIB_00005	GAGGGAATGTATTCTGGAATAGANGAATGTATTAGT AACAAACCCTTGGGTAATACAGAGTGCATACTGGT	<u>244</u>	Influenza B virus
PBIB_00006	CTACCGTGTGGGAGTAGCCGCACTAGGTATCAAAA ACATTGGAAACAAAGAATACTTATGGGATGGACT	<u>245</u>	Influenza B virus

seqid	sequence (5'-3')	SEQ ID NO:	species
PBIB_00007	GGCTATGACTGAAAGAATAACCAGAGACAGCCCAAT TTGGTTCCGGGATTTTTGTAGTATAGCACCGGTC	<u>246</u>	Influenza B virus
PBIB_00008	ACTGATCAGAGGAACATGATTCTTGAGGAACAATGC TACGCTAAGTGTGCAACCTTTTTGAGGCCTGTT	<u>247</u>	Influenza B virus
PBIB_00009	AAAATCCCTTTGTNGGACATTTGTCTATTGAGGGCA TCAAAGANGCAGATATAACCCCAGCACATGGTCC	<u>248</u>	Influenza B virus
PBIB_00010	CTTGGAATACAAGGGAATACAACCTTAAACAAATGC TGAAGACATAGGAACCAAAGGCCAAATGTGCTCA	<u>249</u>	Influenza B virus
PBIB_00011	GTGGCAGGAGCAACATCAGCTGAGTTCATAGAAATG CTACACTGCTTACAAGGTGAAAATTGGAGACAAA	<u>250</u>	Influenza B virus
PBIB_00012	GGAACCCATCCCCGGAAGAGCAACCACAAGCAGTG AAGCTGATGTCGGAAGGAAAACCCAAAAGAAACA	<u>251</u>	Influenza B virus
PBIB_00013	CTGTTTCCAAAGATCAAAGGCACTAAAAAGAGTTGG ACTTGACCCTTCATTAATCAGTACCTTTGCAGGA	<u>252</u>	Influenza B virus
PBIB_00014	AGAGTTTTGTCTGCATTAACAGGCACAGAATTCAAG CCTAGATCAGCATTAATGCAAGGGTTTCCATG	<u>253</u>	Influenza B virus
PBIB_00015	GAGGGACGTGATGCAGATGTCAAAGGAAATCTACTC AAGATGATGAATGACTCAATGGCTAAGAAAACCA	<u>254</u>	Influenza B virus
PBIB_00016	CCTATCAGGAATGGGAACAACAGCAACAAAAAAGAA AGGCCGTATTCTAGCTGAGAGAAAAATGAGAAGA	<u>255</u>	Influenza B virus
PBIB_00017	GCAAGTCAAAGAATGGGGAAGGAATTGCAAAGGAT GTAATGGAAGTGCTAAAGCAGAGCTCTATGGGAA	<u>256</u>	Influenza B virus
PBAd_00001	CTGACACCTACCAAGGTATAAAATCAAACGGAAACG GTAATCCTCAAACTGGACCAAAAATGACGATTT	<u>257</u>	Human adenovirus
PBAd_00002	TCCTCTACTCCAACATTGCACTGTACCTGCCTGACA AGCTAAAATACACTCCTACAAATGTGGAAATATC	<u>258</u>	Human adenovirus
PBAd_00003	GCTATCGGAGGCAGAGTACTAAAAAAGACTACTCCC ATGAAACCATGCTACGGATCGTATGCCAGACCTA	<u>259</u>	Human adenovirus
PBAd_00004	AGTATTGTTTTGTACAGTGAGGATGTTAATATGGAA ACTCCTGATACTCACATTTTCATACAAACCAAGCA	<u>260</u>	Human adenovirus
PBAd_00005	GGGAAACGATCTTAGAGTTGACGGGGCTAGCATTAA GTTTGACAGCATTTGTCTTTACGCCACCTTCTTC	<u>261</u>	Human adenovirus
PBAd_00006	TTGCCATTAAAAACCTCCTCCTCCTGCCAGGCTCAT ATACATATGAATGGAACCTCAGGAAGGATGTTAA	<u>262</u>	Human adenovirus
PBAd_00007	TTGCAACACGTAATGAAATAGGAGTGGGTAACAACT TTGCCATGGAAATTAACCTAAATGCCAACCTATG	<u>263</u>	Human adenovirus



seqid	sequence (5'-3')	SEQ ID NO:	species
PBA <sub>d</sub> _00008	TTGGGGTAAC TGACACCTATCAAGCTATTAAGGCTA ATGGCAATGGCTCAGGCGATAATGGAGATATTAC	<u>264</u>	Human adenovirus
PBA <sub>d</sub> _00009	AGGTATCAAGGCATTAAAGTTAAAACCGATGACGCT AATGGATGGGAAAAGATGCTAATGTTGATACAG	<u>265</u>	Human adenovirus
PBA <sub>d</sub> _00010	GAGAAGTTTTCTGTACTCCAATGTGGCTTTGTACCT TCCAGATGTTTACAAGTACACGCCACCTAACATT	<u>266</u>	Human adenovirus
PBA <sub>d</sub> _00011	ATCAGTCATTTAACGACTACCTCTCTGCAGCTAACA TGCTTTACCCCATTCCTGCCAATGCAACCAACAT	<u>267</u>	Human adenovirus
PBA <sub>d</sub> _00012	CTACTTCGTATATTCTGGATCTATTCCCTACCTGGA TGGCACCTTTTACCTTAACCACACTTTCAAGAAG	<u>268</u>	Human adenovirus
PBA <sub>d</sub> _00013	ACCTGCCAGTGGAAAGGATGCTAACAGCAAAATGCAT ACCTTTGGGGTAGCTGCCATGCCAGGTGTTACTG	<u>269</u>	Human adenovirus
PBA <sub>d</sub> _00014	ATAGAAGCTGATGGGCTGCCTATTAGAATAGATTCA ACTTCTGGAAC TGACACAGTAATTTATGCTGATA	<u>270</u>	Human adenovirus
PBA <sub>d</sub> _00015	TTGAAATTAAGCGCACCGTGGACGGCGAGGGGTACA ACGTGGCCCAAGTGAACATGACCAAGGACTGGTT	<u>271</u>	Human adenovirus
PBA <sub>d</sub> _00016	CGGCAACGACCGGCTCCTGACGCCCAACGAGTTTGA AATTAAGCGCACCGTGGACGGCGAGGGGTACAAC	<u>272</u>	Human adenovirus
PBA <sub>d</sub> _00017	CTCCAGTAAC TTTATGTCCATGGGCGCACTCACAGA CCTGGGCCAAAACCTTCTCTACGCCAACTCCGCC	<u>273</u>	Human adenovirus
PBA <sub>d</sub> _00018	GCTAACTTCCCTATCCGCTTATAGGCAAGACCGCA GTTGACAGCATTACCCAGAAAAAGTTCTTTGCG	<u>274</u>	Human adenovirus
PBA <sub>d</sub> _00019	ACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAA ACACCTACGACTACATGAACAAGCGAGTGGTGGC	<u>275</u>	Human adenovirus
PBA <sub>d</sub> _00020	AAGATGAAC TTTCAAATTACTGCTTTTCCACTGGGAG GTGTGATTAATACAGAGACTCTTACCAAGGTAAA	<u>276</u>	Human adenovirus
PBA <sub>d</sub> _00021	AGCTAACATGC TTTACCCCATCCCTGCCAATGCAAC CAACATTTCAA TTTCCATCCCATCTCGCAACTGG	<u>277</u>	Human adenovirus
PBA <sub>d</sub> _00022	TTCAACTCTTGAAGCCATGCTGCGCAACGATACCAA TGATCAGTCATTCAACGACTACCTCTCTGCAGCT	<u>278</u>	Human adenovirus
PBA <sub>d</sub> _00023	AGGCTGTGGACAGCTATGATCCCGATGTTTCGTATTA TTGAAAATCATGGCGTCGAGGATGAACTGCC TAA	<u>279</u>	Human adenovirus
PBA <sub>d</sub> _00024	TGAAATTTGTGCTTTACACGGAAAATGTCAATTTGGA AACTCCAGACAGCCATGTGGTATACAAGCCAGGA	<u>280</u>	Human adenovirus
PBA <sub>d</sub> _00025	CATCGGCTATCAGGGCTTCTACATTCCAGAAGGATA CAAAGATCGCATGTATTTCATTTTTCAGAACTTC	<u>281</u>	Human adenovirus

seqid	sequence (5' - 3')	SEQ ID NO:	species
PBAd_00026	GCTGCTTCTCCCAGGCTCCTACACTTATGAGTGGAA CTTTAGGAAGGATGTGAACATGGTTCTACAGAGT	<u>282</u>	Human adenovirus
PBAd_00027	ATGACACCAATGATCAGTCATTCAACGACTACCTAT CTGCAGCTAACATGCTCTACCCCATTCCTGCCAA	<u>283</u>	Human adenovirus
PBAd_00028	CTTGCCAACTACAACATTGGATACCAGGGCTTCTAC GTTCTTGAGGGTTACAAGGATCGCATGTACTCCT	<u>284</u>	Human adenovirus
PBAd_00029	GATCGCATGTACTCCTTCTTCAGAACTTCCAGCCC ATGAGTAGACAGGTGGTTGATGAGATTAACATA	<u>285</u>	Human adenovirus
PBAd_00030	CCCCTAAGGGCGCTCCCAATACATCTCAGTGGATTG CTGAAGGCGTAAAAAAGAAGATGGGGGATCTGA	<u>286</u>	Human adenovirus
PBAd_00031	AGAAAAATGTAAATTTGGAACTCCAGATTCCCATGT TGTTTACAAAGCAGGAACCTTCAGACGAAAGCTCT	<u>287</u>	Human adenovirus
PBAd_00032	TGTGGCTACCAATACTGTTTACCAAGGTGTTAAGTT ACAACTGGTCAAACCTGACAAATGGCAGAAAGAT	<u>288</u>	Human adenovirus
PBAd_00033	CCGAATTGGGAAGGGTAGCGTATTCGCCATGGAAAT CAATCTCCAGGCCAACCTGTGGAAGAGTTTCTG	<u>289</u>	Human adenovirus
PBAd_00034	TTGATGAGGTCAATTACAAAGACTTCAAGGCCGTCG CCATACCTACCAACACAACACTCTGGCTTTGT	<u>290</u>	Human adenovirus
PBAd_00035	TGACGAAGAGGAAGAGAAAAATCTCACCCTTACAC TTTGGAAATGCCCCAGTGAAAGCAGAAGGTGGT	<u>291</u>	Human adenovirus
PBAd_00036	AGAAGATTTTGACATTGACATGGCTTTCTTTGATT CAACACTATTAAACACACCAGATGTTGTGCTGTAT	<u>292</u>	Human adenovirus
PBS10062	CTCACATCCTAGGAAGATGCATAGTTTTAGATGTTA AAGGTGTAGAAGAATTGCATGACGATTTAGTTAA	<u>293</u>	HCoV-OC43
PBS10063	GGATTGGCCATTGCACCATAGCTCAACTCACGGATG CAGCACTGTCCATTAAAGGAAAATGTTGATTTTAT	<u>294</u>	HCoV-OC43
PBS10064	GCATGCAATTCAATTATAAAATCACCATCAACCCCT CATCACCGGCTAGACTTGAAATAGTTAAGCTCGG	<u>295</u>	HCoV-OC43
PBS10065	ATAGTTAGTCACTGGATGGGAATTCGTTTTGAATAC ACATCACCCACTGATAAGCTAGCTATGATTATGG	<u>296</u>	HCoV-OC43
PBS10049	AATGGGGTTATGT'TGGTTCACTCTCCACTAATCACC ATGCAATTTGTAATGTTTCATAGAAATGAGCATGT	<u>297</u>	HCoV-229E
PBS10050	GTGTATGACTGCTTTGTTAAGAATGTGGATTGGTCA ATTACCTACCCATGATAGCTAATGAAAATGCCA	<u>298</u>	HCoV-229E
PBS10051	TTGCATCTTCTTTTGTGGTATGCCATCTTTTGTG CATATGAAACAGCAAGACAAGAGTATGAAAATGC	<u>299</u>	HCoV-229E

seqid	sequence(5'-3')	SEQ ID NO:	species
PBS10052	AAATGGTTCCTCACCACAAATAATCAAACAATTGAA GAAGGCTATGAATGTTGCAAAAGCTGAGTTTGAC	<u>300</u>	HCoV-229E
PBS10053	CTGCTGCAGCTATGTACAAAGAAGCACGTGCTGTTA ATAGAAAATCAAAGTTGTTAGTGCCATGCATAG	<u>301</u>	HCoV-229E
PBS10054	ACGTTTGGACATGTCTAGTGTGACACTATCCTTAA TATGGCACGTAATGGTGTGTCCCTCTTTCCGTT	<u>302</u>	HCoV-229E
PBS10055	CTGGTGGTAAAGTTTCATTTTCTGATGACGTTGAAG TAAAAGACATTGAACCTGTTTACAGAGTCAAGCT	<u>303</u>	HCoV-229E
PBS10056	TTTACAGAGTCAAGCTTTGCTTTGAGTTTGAAGATG AAAACTTGTAGATGTTTGTGAAAAGGCAATTGG	<u>304</u>	HCoV-229E
PBS10057	GATGTTTGTGAAAAGGCAATTGGCAAGAAAATTAAA CATGAAGGTGACTGGGATAGCTTTTGTAAAGACTA	<u>305</u>	HCoV-229E
PBS10058	GCGTTGTTGGCCTTTTTCTTGTCTAAGCATAGTGAT TTTGGTCTTGGTGATCTTGTGCGATTCTTATTTTG	<u>306</u>	HCoV-229E
PBS10059	AGCAAGACAAGAGTATGAAAATGCTGTTGCAAATGG TTCTCACCACAAATAATCAAACAATTGAAGAAG	<u>307</u>	HCoV-229E
PBS10060	TTGAAGAAGGCTATGAATGTTGCAAAAGCTGAGTTT GACAGGGAATCATCTGTTCAAAGAAAATTAAACA	<u>308</u>	HCoV-229E
PBS10061	CTGCTGCAGCTATGTACAAAGAAGCACGTGCTGTTA ATAGAAAATCAAAGTTGTTAGTGCCATGCATAG	<u>309</u>	HCoV-229E
PBHE_00001	CGGGATAAGGCACTCTCTATCAGAATGGATGTCTTG CTGCTATAATAGATAGAGAAGGTTATAGCAGACT	<u>310</u>	Human enteric coronaviruse
PBHE_00002	CCCTCGCAGGAAAGTCGGGATAAGGCACTCTCTATC AGAATGGATGTCTTGCTGCTATAATAGATAGAGA	<u>311</u>	Human enteric coronaviruse
PBHE_00003	ATGGATGTTTTGAGGACGCAGAGGAGAAGTTGGACAA CCCTAGTAGTTCAGAGGTGGATATAGTATGCT	<u>312</u>	Human enteric coronaviruse
PBHE_00004	CCTTGGGTATGTACTTGCCTAAGTGTGGCGAAAAG GGTGCCCTACAATAAAGATCATAAACGTGTCCG	<u>313</u>	Human enteric coronaviruse
PBHE_00005	GGGGATGCTGGTTTTACTAGCATACTCAGTGGTTTTG TTATATGATTCACCTGTTTTTCACAGCAAGG	<u>314</u>	Human enteric coronaviruse
PBHE_00006	CATGACGGCAGTTGCTTGTCAACCCCCGTACTGTTA TTTTTCGTAATTCTACTACCAACTATGTTGGTG	<u>315</u>	Human enteric coronaviruse
PBRh_00001	GGCTGAGTGATTACATCAGGTTTGGGTAGAGCTT TTGGTGTCCGGTTCCTGACCAAATCTCAACAAA	<u>316</u>	Human rhinovirus
PBRh_00002	GAAAAGCTATTAGCTTGGTAGACAGAACTACCAACG TTAGGTATAGTGTGGATCAACTGGTCACGGCTAT	<u>317</u>	Human rhinovirus

seqid	sequence (5'-3')	SEQ ID NO:	species
PBRh_00003	GGCCAAGTAATAGCTAGACATAAGGTTAGGGAGTTT AACATAAATCCAGTCAACACGGCAACTAAGTCAA	<u>318</u>	Human rhinovirus
PBRh_00004	GATAACAAGGGCATGTTATTTCACCAGTAATTTTGTT CTAGCCTCCACAAATTCTAACACACTAAGCCCCC	<u>319</u>	Human rhinovirus
PBRh_00005	GGCCAAGAAGTAAGGTTGTGTTTAGTACCACTCAGG GTTTACCAGTTATGTTAACACCTGGATCTGGGCA	<u>320</u>	Human rhinovirus
PBRh_00006	GTAATGCGTAAGTGCGGGATGGGACCAACTACTTTG GGTGTCCGTGTTTCCTGTTTTCTTTTGATTGCA	<u>321</u>	Human rhinovirus
PBRh_00007	TAAAAGAGGATTCAGAGCTGATGAGCGCCACTCTTT CCTTATACACCCTACCTTTCCTGTGGCTGAGATT	<u>322</u>	Human rhinovirus
PBRh_00008	GCAAGTTTTCATCAGGGTTTATTAATAGTTGCCGCCA TCCCAGAACATCAATTGGCATCTGCAACAAGTGG	<u>323</u>	Human rhinovirus
PBMP_00001	ATATATGAAGGAACACCAGTGGCGAAGGCGAAAAC TAGGCCATTACTGACGCTTAGGCTTGAAAGTGTG	<u>324</u>	Mycoplasma pneumoniae
PBMP_00002	GCAGTAGGGAATTTTTCACAATGAGCGAAAGCTTGA TGGAGCAATGCCGCGTGAACGATGAAGGTCTTTA	<u>325</u>	Mycoplasma pneumoniae
PBMP_00003	AACACATTAAGTATCTCGCCTGGGTAGTACATTCGC AAGAATGAAACTCAAACGGAATTGACGGGGACCC	<u>326</u>	Mycoplasma pneumoniae
PBMP_00004	ACACCGTAAACGATAGATACTAGCTGTCGGGGCGAT CCCCTCGGTAGTGAAGTTAACACATTAAGTATCT	<u>327</u>	Mycoplasma pneumoniae
PBMP_00005	ACATCCTTGGCAAAGTTATGGAACATAATGGAGGT TAACCGAGTGACAGGTGGTGCATGGTTGTCGTCA	<u>328</u>	Mycoplasma pneumoniae
PBR_00001	TTATAACTTAACCGTCGGCAGTTGGGTAAAGAGACCA CGTCCGATCAATTGTGCGAGGGCGCGTGGGAAGTG	<u>329</u>	Rubella virus
PBR_00002	ATACCCAGACCTGTGTTTCACGCAGATGCAGGTCAGT GATCACCCAGCACTCCACGCAATTTTCGCGGTATA	<u>330</u>	Rubella virus
PBR_00003	AGAAACTCCTAGATGAGGTTCTTGCCCCCGGTGGGC CTTATAACTTAACCGTCGGCAGTTGGGTAAAGAGA	<u>331</u>	Rubella virus
PBR_00004	ATACCCAGACCTGTGTTTCACGCAGATGCAGGTCAGT GATCACCCAGCACTCCACGCAATTTTCGCGGTATA	<u>332</u>	Rubella virus
PBR_00005	TCTTACTTCAACCCTGGCGGCAGCTACTACAAGCAG TACCACCCTACCGCGTGCAGGTTGAACCT	<u>333</u>	Rubella virus
PBM_00001	AAGGCTTGTTTCAGAGATTGCAATGCATACTACTGA GGACAGGATCAGTAGAGCAGTTGGACCCAGACAA	<u>334</u>	Measles virus
PBM_00002	AGGATCAGTAGAGCAGTTGGACCCAGACAAGCCCAA GTGTCAATTCCTACACGGTGATCAAAGTGAGAATG	<u>335</u>	Measles virus

seqid	sequence (5' - 3')	SEQ ID NO:	species
PBM_00003	TCAGTAGAGCAGTTGGACCCAGACAAGCCCAAGTGT CATTCCTACACGGTGATCAAAGTGAGAATG	<u>336</u>	Measles virus
PBM_00004	CCCAGGGAATGTACGGGGGAACCTTACCTAGTTGAAA AGCCTAATCTGAGCAGCAAAGGATCAGAATTATC	<u>337</u>	Measles virus
PBM_00005	CCCAGGGAATGTACGGGGGAACCTTACCTAGTTGAAA AGCCTAATCTGAGCAGCAAAGGATCAGAATTATC	<u>338</u>	Measles virus
PBRSV_00001	CAAACCCACAAACAAACCAACCACCAAAAACCACAAA CAAAAGAGACCCAAAAACACCAGCCAAAACGACG	<u>339</u>	Human respiratory syncytial virus
PBRSV_00002	GCAGCACTTGTAATAACCAAATTAGCAGCAGGAGAC AGATCAGGTCTTACAGCAGTAATTAGGAGGGCAA	<u>340</u>	Human respiratory syncytial virus
PBRSV_00003	CAAGAGGGGGTAGTAGAGTTGAAGGAATCTTTGCAG GATTGTTTATGAATGCCTATGGTTCAGGGCAAGT	<u>341</u>	Human respiratory syncytial virus
PBRSV_00004	GACTTAACAGCAGAAGAATTGGAAGCCATAAAGAAT CAACTCAACCCTAAAGAAGATGATGTAGAGCTTT	<u>342</u>	Human respiratory syncytial virus
PBRSV_00005	TCACAATCCACTGTGCTCGACACAACCACATTAGAA CACACAATCCAACAGCAATCCCTCCACTCAACCA	<u>343</u>	Human respiratory syncytial virus
PBRSV_00006	GACTTAACAGCAGAAGAATTGGAAGCCATAAAGAAT CAACTCAACCCTAAAGAAGATGATGTAGAGCTTT	<u>344</u>	Human respiratory syncytial virus
PBPI_00001	GCCGACGACCATCAAGCGTAGCCAAACAAGATCAGA GAGAACACAGAATTCAGAACTCCACAAATCAACA	<u>345</u>	Parainfluenza
PBPI_00002	CGACCCAAGATCATAGATCAAGTGAGGAGAGTGGA TCTCTAGGAGAACAGGTGAGTCAAAAAC TGAGAC	<u>346</u>	Parainfluenza
PBPI_00003	CGCAATGAAGAGGGAACCAGCAACACATCAGTCGA TGAGATGGCCAAGTTACTAGTAAGTCTTGGTGTA	<u>347</u>	Parainfluenza
PBPI_00004	CTCCTTGCAATGGCCATACGTAGTCCGGAATTATAT CTCACTACAAACGGTGTCAATGCTGATGTCAAGT	<u>348</u>	Parainfluenza
PBPI_00005	GAACAAAAACAGATGGGTTTCATTGTCAAAAACGAGAG ACATGGAGTATGAAAGAACCACAGAGTGGTTGTT	<u>349</u>	Parainfluenza
PBPI_00006	TGTTCCAAGGGCAAAGAGAGAATGCGGATCTAGAGG CATTGCTTCAGACATATGGATATCCTGCATGTC	<u>350</u>	Parainfluenza
PBPI_00007	GGTATATCCCTCTTCCAGCCACATCATGACAAAAG GGGCATTTCTAGGTGGAGCAGATATCAAAGAATG	<u>351</u>	Parainfluenza

seqid	sequence (5'-3')	SEQ ID NO:	species
PBPI_00008	GTATAACAACCACATGTACATGCAACGGTATTGGCA ATAGAATCAATCAACCACCTGATCAAGGAGTAAA	<u>352</u>	Parainfluenza
PBPI_00009	CCCAACCCATTCAAAACGAAAATCTCAAAAAGAGATT GGCAACACAACAAACACTGAACATCATGCCAACC	<u>353</u>	Parainfluenza
PBME_00001	AAAAGTGTATCACAGAAGTTTGTTCATTGAGTATGG CAAAGCATTAGGCTCATCATCTACAGGCAGCAAA	<u>354</u>	Human metapneumovirus
PBME_00002	GAAAGTCTATTTGTTAATATATTCATGCAAGCTTAT GGAGCCGGTCAAACAATGCTAAGGTGGGGGTCA	<u>355</u>	Human metapneumovirus
PBME_00003	ACGCTGTTGTGTGGAGAAATTCTGTATGCTAAACAT GCTGATTACAAATATGCTGCAGAAATAGGAATAC	<u>356</u>	Human metapneumovirus
PBME_00004	TTAAGGAATCATCAGGTAATATCCCACAAAATCAGA GGCCCTCAGCACCAGACACCCATAATCTTATT	<u>357</u>	Human metapneumovirus
PBME_00005	TGAGCAATCAAAGGAGTGCAACATCAACATATCCAC TACAAATTACCCATGCAAAGTCAGCACAGGAAGA	<u>358</u>	Human metapneumovirus
PBME_00006	CTGTTCCATTGGCAGCAACAGAGTAGGGATCATCAA GCAGCTGAACAAAGGTTGCTCCTATATAACCAAC	<u>359</u>	Human metapneumovirus
PBME_00007	ACTTAATGACAGATGCTGAACTAGCCAGGGCCGTTT CTAACATGCCGACATCTGCAGGACAAATAAAATT	<u>360</u>	Human metapneumovirus
PBME_00008	AAAAAAAGGGAAACTATGCTTGCCTCTTAAGAGAAG ACCAAGGTGGTATTGTGTCAGAATGCAGGGTCAAC	<u>361</u>	Human metapneumovirus
PBME_00009	GAAAAGAACACACCAGTTACAATACCAGCATTATC AAATCGGTTTCTATCAAAGAGAGTGAATCAGCCA	<u>362</u>	Human metapneumovirus
PBME_00010	CAAATCAGTTGGCAAAAAACACATGATCTGATCGC ATTATGTGATTTTATGGATCTAGAAAAGAACACA	<u>363</u>	Human metapneumovirus
PBME_00011	CAGCTAAAGACACTGACTATAACTACTCTGTATGCT GCATCACAAGTGGTCCAATACTAAAAGTGAATG	<u>364</u>	Human metapneumovirus
PBME_00012	AAAAGAACACACCAGTTACAATACCAGCATTATCA AATCGGTTTCTATCAAAGAGAGTGAATCAGCCAC	<u>365</u>	Human metapneumovirus
PBME_00013	CTATTATAGGAGAAAAAGTGAACACTGTATCTGAAA CATTGGAATTACCTACTATCAGTAGACCCACCAA	<u>366</u>	Human metapneumovirus
PBME_00014	AAGTTAGCATGGACAGACAAAGGTGGGGCAATCAA ACTGAAGCAAAGCAAACAATCAAAGTTATGGATC	<u>367</u>	Human metapneumovirus
PBME_00015	CAGGAAAATACACAAAGTTGGAGAAAAGATGCTCTAG ACTTGCTTTCAGACAATGAAGAAGAAGATGCAGA	<u>368</u>	Human metapneumovirus
PBME_00016	CTAATAGCAGACATAATAAAAGAAGCCAAGGGAAAA GCAGCAGAAATGATGGAAGAAGAAATGAACCAGC	<u>369</u>	Human metapneumovirus

seqid	sequence (5' - 3')	SEQ ID NO:	species
PBCP_00001	ACCCTTATCGTTAGTTGCCAGCACTTAGGGTGGGAA CTCTAACGAGACTGCCTGGGTAAACCAGGAGGAA	370	Chlamydophila pneumoniae
PBCP_00002	ATAAGAGAGGTTGGCTAATATCCAATTGATTTGAGC GTACCAGGTAAAGAAGCACCGGCTAACTCCGTGC	371	Chlamydophila pneumoniae
PBCP_00003	CATGGGATCTTAAGTTTTAGTTGAATACTTCTGGAA AGTTGAACGATACAGGGTGATAGTCCCGTAAACG	372	Chlamydophila pneumoniae
PBCP_00004	GGGTGCTAGCGTTAATCGGATTTATTGGGCGTAAAG GGCGTGTAGGCGGAAAGGAAAGTTAGATGTTAAA	373	Chlamydophila pneumoniae
PBCP_00005	GCCAGGGAGTTAAGTTAAACGGCGAGATTAAGGGAT TTACATTCCGGAGTCGAAGCGAAAGCGAGTTTTA	374	Chlamydophila pneumoniae
PBCP_00006	GCCAGGGAGTTAAGTTAAACGGCGAGATTAAGGGAT TTACATTCCGGAGTCGAAGCGAAAGCGAGTTTTA	375	Chlamydophila pneumoniae

Please replace Table 16, beginning on page 38 and bridging to page 42, with a new Table 16 as follows:

Table 16. Exemplary probes for non-SARS-CoV infectious organisms damaging host's immune system

id	sequence (5' - 3')	SEQ ID NO:	species
PBHAV_00001	GGTGTGAACCTGAGAAAAATATTTACACCAAACCTGTGGC CTCAGATTATTGGGATGGATATAGTGGAC	376	HAV
PBHAV_00002	ACTGAGGAGCATGAAATAATGAAGTTTTCTTGGAGAGGAGT GACTGCTGATACTAGGGCTTTTGAGAAGAT	377	HAV
PBHAV_00003	CATGGCGTGACTAAGCCCAAACAAGTGATTAAATTGGATGC AGATCCAGTAGAGTCCCAGTCAACTCTAG	378	HAV
PBHAV_00004	GTGCAGTGATGGACATTACAGGAGTGACAGTCAACCTTGAGA TTTCGTGTTCCCTTGGATTTCTGATACACC	379	HAV
PBHAV_00005	CCAAAAGAGATTTAATTTGGTTGGATGAAAATGGTTTGCTG TTAGGAGTTCACCCAAGATTGGCCCAGAG	380	HAV
PBHAV_00006	AGAGATGCTTTGGATAGGGTAACAGCGGCGGATATTGGTGA GTTGTTAAGACAAAACCATTCACGCCG	381	HAV
PBHBV_00001	GCTGGATGTGCTGCGGCGTTTTATCATATTCCTCTTCATC CTGCTGCTATGCCTCATCTTCTTATTGGT	382	HBV
PBHBV_00002	ATATACATCCTTTCCATAGCTGCTAGGTTGTACTGCCAACT AGATTCTTCGCGGGACGTCCTTTGTCTAC	383	HBV
PBHBV_00003	ATTCTTTCCCGATCATCAGTTGGACCCTGCATTCCGAGCCA ATTCAAACAATCCAGATTGGGACTTCAAC	384	HBV

id	sequence (5' - 3')	SEQ ID NO:	species
PBHBV_00004	CTCATGTTGCTGTACAAAACCTACGGATGGAAATTGCACCT GTATTCCCATCCCATCATCTTGGGCTTTC	385	HBV
PBHBV_00005	AGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTCTAGGG GGAGCACCCGTGTGTCCTGGCCAAAATTC	386	HBV
PBHBV_00006	CCTTGGATGGCTTTGGGGCATGGACATTGACCCTTATAAAG AATTGGAGCTACTGTGGAGTTACTCTCA	387	HBV
PBHCV_00001	TGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGG CAACATAATCATGTTTGCCCCACACTGT	388	HCV
PBHCV_00002	TGAGCGACTTTAAGACCTGGCTGAAAGCCAAGCTCATGCCA CAACTGCCTGGGATTCCCTTTGTGT	389	HCV
PBHCV_00003	TATAGATGCCCACTTTCTATCCCAGACAAAGCAGAGTGGGG AGAACTTTCCTTACCTGGTAGCGTACCAA	390	HCV
PBHCV_00004	TAACAACACCAGGCCACCGCTGGGCAATTGGTTCGGTTGTA CCTGGATGAACCAACTGGATTACCAAA	391	HCV
PBHCV_00005	TTTATCCCTGTGGAGAACCTAGAGACAACCATGAGATCCCC GGTGTTACGGACAACCTCTCCACCAG	392	HCV
PBHCV_00006	TTTATCCCTGTGGAGAACCTAGAGACAACCATGAGATCCCC GGTGTTACGGACAACCTCTCTCCACCAG	393	HCV
PBHDV_00001	TTCCCTTCTCTCGTCTTCCTCGGTCAACCTCTTAAGTTCCT CTTCTTCTTCCTTGCTGAGGTGCTTCCCT	394	HDV
PBHDV_00002	TAAGCCCATAGCGATAGGGAGAGATGCTAGGAGTTAGAGGA GACCGAAGCGAGGAGGAAAGCAAAGAGAG	395	HDV
PBHDV_00003	TTGGAGAGCACTCCGGCCGAAAGGTGAGGTACCCAGAAGG AGGAATCTCACGGAGAAAAGCAGACAAAT	396	HDV
PBHDV_00004	TTAAGTTCCTCTTCTTCTTCCTTGCTGAGGTGCTTCCCTCC CGCGCCAGCTGCTTTCTCTTGTTCTCGA	397	HDV
PBHDV_00005	AAAAAGAGAAAGCAAGAGACGGACGATTTCCTCCATGACTCT GGAGACATCCTGGAAGGGGAAAGAAGGAA	398	HDV
PBHDV_00006	AAGTTCCTCTTCTTCTTCCTTGCTGAGGTGCTTCCCTCCCG CGGCCAGCTGCTTTCTCTTGTTCTCGAGG	399	HDV
PBHGV_00001	TCATATCATGCATCATTTGGACACGGCCCCCTTCTGCTCCAC TTGGCTTGCTGAGTGCAATGCAGAT	400	HGV
PBHGV_00002	TAAAGTGGGAAAGTGAGTTTTGGAGATGGACTGAACAGCTG GCCTCCAACACTAGGATTCTGGAATACCT	401	HGV
PBHGV_00003	TAGGTCGTAAATCCCGGTCACCTTGGTAGCCACTATAGGTG GGTCTTAAGAGAAGGTTAAGATTCTCTT	402	HGV



id	sequence (5' - 3')	SEQ ID NO:	species
PBHG_V_00004	TTCTTGGTTTGCCTCCACCAGTGGTCGCGACTCGAAGATAG ATGTGTGGAGTTTAGTGCCAGTTGG	<u>403</u>	HGV
PBHG_V_00005	TCCAAC TACTGGATTCTGGAATACCTCTGGAAGGTCCCATT TGATTTCTGGAGAGGCGTGATAAGCCTGA	<u>404</u>	HGV
PBHG_V_00006	ACGTTACCAAGGTCCTTCATGTATCCCGGACAGTTACTTTCA GCAAGTTGACTATTGCGACAAGGTCTCAG	<u>405</u>	HGV
PBTTV_00001	TGTCAGTAACAGGGGTCGCCATAGACTTCGGCCTCCATTTT ACCTTGTA AAAACTACCAAAATGGCCGTT	<u>406</u>	TTV
PBTTV_00002	ATGTCATCCATTTCTTGGGCCGGGTCTACGTCTCATATAA GTAAGTGCAGTTCCGAATGGCTGAGTTTT	<u>407</u>	TTV
PBTTV_00003	GGGATCTAGCATCCTTATTTCAAATAGCACCATAAACATGT TTGGTGACCCCAAACCTTACAACCTTCC	<u>408</u>	TTV
PBTTV_00004	TGTTAGAAATCCCTGCAAAGAAACCCACTCCTCGGGCAATA GAGTCCCTAGAAGCTTACAAATCGTTGAC	<u>409</u>	TTV
PBTTV_00005	TCAAGGATTGACGTAAAGGTTAAAGGTCATCCTCGGCGGAA GCTACACAAAATGGTGGACAACATCTTCC	<u>410</u>	TTV
PBB19_00001	GGCATGGTTAACTGGAATAATGAAAACCTTTCCATTTAATGA TGTAGCAGGGAAAAGCTTGGTGGTCTGGG	<u>411</u>	B19
PBB19_00002	GGCAAGAAAAATACACTGTGGTTTTATGGGCCGCCAAGTAC AGGAAAAACAACTTGGCAATGGCCATTG	<u>412</u>	B19
PBB19_00003	GCCATTTCTCATGGTCAGACCACTTATGGTAACGCTGAAGA CAAAGAGTATCAGCAAGGAGTGGGTAGAT	<u>413</u>	B19
PBB19_00004	AATTTTCGAGAATTTACCCCAAGATTTGGTGCGGTGTAGCTGC CATGTGGGAGCTTCTAATCCCTTTTCTGT	<u>414</u>	B19
PBHCMV_00001	AGGTGCGCAACGCTTTTATGAAGGTAAAGCCCGTGGCCCAG GAGATTATCCGTATCTGCATACTCGCTAA	<u>415</u>	HCMV
PBHCMV_00002	TAAACGACATGTATCTGTTGTTGACGCTGCGACACTTGCAG CTGCGACACGCGCTGGAGCTACAAATGAT	<u>416</u>	HCMV
PBHCMV_00003	CAAAGCAGCGTCAACAACAGCCACACAGAAACCTACGTGGA GACGACACGGGACTTTTTATTGACGGAGA	<u>417</u>	HCMV
PBHCMV_00004	TGCTCCAAAGCAGCGTCAACAACAGCCACACAGAAACCTAC GTGGAGACGACACGGGACTTTTTATTGAC	<u>418</u>	HCMV
PBEV_00001	GAGTTAAAAGCAACTACTGTTTATTTTCCAAAATGAGCTGG GTATAGTTGATGATCTGTAGGCGCAGCTC	<u>419</u>	EBV
PBEV_00002	ACAGTGACAGTGGGAGAAACACGGCCTCTGAGACATGTATG GGGGTGTTCATCTCACGCAGAAAATCTTT	<u>420</u>	EBV

id	sequence(5'-3')	SEQ ID NO:	species
PBEV_00003	TGAAGAAGTCCCGTAGTGAAAAATGGGATCTGTCTACACCA TGTCTGGTGTGCCGGGAACATATTGATCG	<u>421</u>	EBV
PBEV_00004	TGAAGAAGTCCCGTAGTGAAAAATGGGATCTGTCTACACCA TGTCTGGTGTGCCGGGAACATATTGATCG	<u>422</u>	EBV
PBHIV1_00001	ATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGCTGA GGGCTATTGAGGCGCAACAGCATCTGTTG	<u>423</u>	HIV1
PBHIV1_00002	GCAACCCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGA CACCAAGGAAGCTTTAGACAAGATAGAGG	<u>424</u>	HIV1
PBHIV1_00003	TGTATGTAGGATCTGACTTAGAAATAGGGCAGCATAGAACA AAATAGAGGAGCTGAGACAACATCTGTT	<u>425</u>	HIV1
PBHIV1_00004	GGAATGCTAGTTGGAGTAATAAATCTCTGGAACAGATTTGG AATCACACGACCTGGATGGAGTGGGACAG	<u>426</u>	HIV1
PBTP_00001	TACCTTGAAAGACGTTACCGCCAAAATGCTCATCAAAAGAA CGAGGACCATGCTGACAGCACCCGCGACA	<u>427</u>	TP
PBTP_00002	TTTCGTGATCCTTTTTCCTTTTTCCTGTAGCTCAGCGTCCTTT TTATCTAATTCTCTGCACGCTCCCCGAG	<u>428</u>	TP
PBTP_00003	TCTTTCTGACTCGCGCAAAAGGCATTACTGGAACACTATTT TAGCCATGTGGTGGCTCCCTGCTATCTTA	<u>429</u>	TP
PBTP_00004	ACCTTGAAAGACGTTACCGCCAAAATGCTCATCAAAAGAAC GAGGACCATGCTGACAGCACCCGCGACAA	<u>430</u>	TP
PBHEV_00001	AATAATTCACGCCGTCGCTCCTGATTATAGGTTGGAACATA ACCCAAAGATGCTTGAGGCTGCCTACCGG	<u>431</u>	HEV
PBHEV_00002	TTTGTTGACGGGGCGGTTTTAGAGACTAATGGCCCAGAGCG CCACAATCTCTCTTTTGATGCCAGTCAGA	<u>432</u>	HEV
PBHEV_00003	ATTTTACTAGTACTAATGGTGTGCGTGAGATCGGCCGCGGG ATAGCGCTTACCCTGTTTAACCTTGCTGA	<u>433</u>	HEV
PBHEV_00004	AGTCCACTTACGGCTCTTCGACCGGCCAGTCTATGTCTCT GACTCTGTGACCTTGGTAAATGTAG	<u>434</u>	HEV

Please replace Table 17, beginning on page 43 and bridging to page 44, with a new Table 17 as follows:

Table 17. Exemplary probes for non-SARS-CoV coronaviridae virus

seqid	sequence (5' -3')	SEQ ID NO:
PBIBV_00001	GGTATAGTGTGGGTTGCTGCTAAGGGTGCTGATACTAAATCTAGATCCAAT CAGGGTACAAGAGATCCTG	<u>435</u>
PBIBV_00002	GGTATAGTGTGGGTTGCTGCTAAGGGTGCTGATACTAAATCTAGATCCAAT CAGGGTACAAGAGATCCTG	<u>436</u>
PBMHV_00001	CCAGCCCAAGCAAGTAACGAAGCAAAGTGCCAAAGAAGTCAGGCAGAAAAT TTTAAACAAGCCTCGCCAA	<u>437</u>
PBMHV_00002	TCTAAACTTTAAGGATGTCTTTTGTTCCTGGGCAAGAAAATGCCGGTGGCA GAAGCTCCTCTGTAAACCG	<u>438</u>
PBEQ_00001	AGGATCAAGAAATAGATCCAATTCCGGCACTAGAACACCCACCTCTGGTGT GACATCTGATATGGCTGAT	<u>439</u>
PBEQ_00002	TTTAAACAGCCGATGGCAATCAACGCCAATTGTTGCCACGCTGGTATTTT TACTACTTGGGAACAGGCC	<u>440</u>
PBCA_00001	TTGGAACCTTATGTCCGAGAGACTTTGTACCCAAAGGAATAGGTAACAAGGA TCAACAGATTGGTTATTGG	<u>441</u>
PBCA_00002	GCTGAATGTGTTCCATCTGTATCTAGCATTCTGTTTGGAAGCTATTGGACT GCAAAGGAAGATGGCGACC	<u>442</u>
PBFE_00001	CACCACCCTCGAACAAGGAGCTAAATTTTGGTATGTATGTCCGAGAGACTT TGTTCCTCAAGGGAATAGGT	<u>443</u>
PBFE_00002	GGCACTCGTGGAACCAACAATGAATCCGAACCATTGAGATTGATGGTAAG ATACCACCACAATTCCAGC	<u>444</u>
PBPEDV_00001	CTGATCCAAATGTTGAGCTTCTTGTGTCACAGGTGGATGCATTTAAACTG GGAATGCAAAACCCAGAG	<u>445</u>
PBPEDV_00002	ATGAGCAAATTCGCTGGCGTATGCGCCGTGGTGAGCGAATTGAACAACCTT CAAAATGGCATTCTACTA	<u>446</u>
PBPTGV_00001	GAGAGACTTTGTACCCAAAGGAATAGGTAACAGGGATCAACAGATTGGTTA TTGGAATAGACAACTCGC	<u>447</u>
PBPTGV_00002	GATGGTGACCAGATAGAAGTCACGTTACACACAAAATACCATTGCCAAAG GATGATCCTAAACTGGAC	<u>448</u>
PBBOV_00001	TATTTTACTATCTTGGAACAGGACCGCATGCCAAAGACCAGTATGGCACC GACATTGACGGAGTCTACT	<u>449</u>
PBBOV_00002	AGAACCCCTACCTCTGGTGTAACACCTGATATGGCTGATCAAATTGCTAGT CTTGTCTGGCTAAACTTG	<u>450</u>
PBFIPV_00001	GAGTGTGGTTAATCAACAGGGTGAAGCGCTGAGTCAACTTACCAGTCAGTT ACAGAAAACTTCCAGGCT	<u>451</u>
PBFIPV_00002	CCGGCATTGTAGATGGTAATAAGATGGCCATGTACACAGCATCTTTAATTG GAGGTATGGCTTTGGGCTC	<u>452</u>

seqid	sequence (5'-3')	SEQ ID NO:
PBR_00001	AAATGTTAAAACTTGGAACTAGTGATCCACAGTTCCCCATTCTTGCAGAGT TGGCCCCAACACCTGGTGC	<u>453</u>
PBR_00002	CCCATTA CTCTTGGTTTTCGGGCATTACCCAATTTCAAAGGGAAAGGAGT TCCAGTTTGCAGATGGGCA	<u>454</u>
PBPHEV_00001	TAGTAACCAGGCTGATATTAATACCCCGGCTGACATTGTCTGATCGGGATCC AAGTAGCGATGAGGCTATT	<u>455</u>
PBPHEV_00002	TTCTTTTAAACAGCCGATGGCAATCAGCGTCAACTGCTGCCACGATGGTA CTTTTACTACCTGGGAACA	<u>456</u>
PBPV_00001	GTGGTTCCCCATTACTCCTGGTTTCTGGCATTACCCAATTCCAGAAGGGA AAGGAGTTTAAGTTTGCAG	<u>457</u>
PBPV_00002	AAGAAGTCAGGCAGAAAATTTTAAACAAGCCTCGCCAAAAGAGGACTCCAA ACAAGCAGTGCCCAAGTCA	<u>458</u>
PBTK_00001	TTTGGTGATGACAAGATGAATGAGGAAGGTATTAAGGATGGGCGTGTTACG GCAATGCTCAACCTAGTCC	<u>459</u>
PBTK_00002	TTTGGTGATGACAAGATGAATGAGGAAGGTATTAAGGATGGGCGTGTTACG GCAATGCTCAACCTAGTCC	<u>460</u>
PBSDAV_00001	AGCCTGCCTCTACTGTAAAACCTGATATGGCCGAAGAAATTGCTGCTCTTG TTTTGGCTAAGCTAGGCAA	<u>461</u>
PBSDAV_00002	CCCCATTCTTGCAGAGTTGGCCCCAACACCTGGTGCCTTCTTCTTTGGATC TAAATTAGAATTGGTCAAA	<u>462</u>

Please replace Table 18, beginning on page 50 and bridging to page 54, with a new Table 18 as follows:

Table 18. Exemplary SARS-CoV primers

id	sequence (5'-3')	SEQ ID NO:	region
PMSL_00005	CACGTCTCCCAAATGCTTGAGTGACG	<u>463</u>	SARS-Cov Nucleocapsid gene
PMSU_00006	CCTCGAGGCCAGGGCGTTCC	<u>464</u>	SARS-Cov Nucleocapsid gene
PMV_00039	TCACTTGCTTCCGTTGAGGTCGGGGACCAAGACC TAATCAGA	<u>465</u>	SARS-Cov Nucleocapsid gene
PMV_00040	GGTTTCGGATGTTACAGCGTAGCCGCAGGAAGAA GAGTCACAG	<u>466</u>	SARS-Cov Nucleocapsid gene
PMV_00041	TCACTTGCTTCCGTTGAGGAGGCCAGGGCGTTCC AATC	<u>467</u>	SARS-Cov Nucleocapsid gene

id	sequence(5'-3')	SEQ ID NO:	region
PMV_00042	GGTTTCGGATGTTACAGCGTCAATAGCGCGAGGG CAGTTTC	<u>468</u>	SARS-Cov Nucleocapsid gene
PMV_00043	TCACTTGCTTCCGTTGAGGGGCACCCGCAATCCT AATAACAA	<u>469</u>	SARS-Cov Nucleocapsid gene
PMV_00044	GGTTTCGGATGTTACAGCGTAGCCGCAGGAAGAA GAGTCACAG	<u>470</u>	SARS-Cov Nucleocapsid gene
PMV_00090	TCGGGGACCAAGACCTAATCAGA	<u>471</u>	SARS-Cov Nucleocapsid gene
PMV_00091	AGCCGCAGGAAGAAGAGTCACAG	<u>472</u>	SARS-Cov Nucleocapsid gene
PMV_00092	AGGCCAGGGCGTTCCAATC	<u>473</u>	SARS-Cov Nucleocapsid gene
PMV_00093	CAATAGCGCGAGGGCAGTTTC	<u>474</u>	SARS-Cov Nucleocapsid gene
PMV_00094	GGCACCCGCAATCCTAATAACAA	<u>475</u>	SARS-Cov Nucleocapsid gene
PMV_00095	AGCCGCAGGAAGAAGAGTCACAG	<u>476</u>	SARS-Cov Nucleocapsid gene
PMSL_00001	ACATCACAGCTTCTACACCCGTTAAGGT	<u>477</u>	SARS-Cov Replicase 1A
PMSL_00002	ATACAGAATACATAGATTGCTGTTATCC	<u>478</u>	SARS-Cov Replicase 1A
PMSU_00002	GCATCGTTGACTATGGTGTCCGATTCT	<u>479</u>	SARS-Cov Replicase 1A
PMSU_00003	GCTGCATTGGTTTGTATATCGTTATGC	<u>480</u>	SARS-Cov Replicase 1A
PMV_00023	TCACTTGCTTCCGTTGAGGAGCCGCTTGTCACAA TGCCAATT	<u>481</u>	SARS-Cov Replicase 1A
PMV_00024	GGTTTCGGATGTTACAGCGTCATCACCAAGCTCG CCAACAGTT	<u>482</u>	SARS-Cov Replicase 1A
PMV_00025	TCACTTGCTTCCGTTGAGGAGGTTGCCATCATTT TGGCATCTT	<u>483</u>	SARS-Cov Replicase 1A
PMV_00026	GGTTTCGGATGTTACAGCGTCTTTGCGCCAGCGA TAGTGACTT	<u>484</u>	SARS-Cov Replicase 1A
PMV_00027	TCACTTGCTTCCGTTGAGGATGGCACCCGTTTCT GCAATGG	<u>485</u>	SARS-Cov Replicase 1A

id	sequence(5'-3')	SEQ ID NO:	region
PMV_00028	GGTTTCGGATGTTACAGCGTTCGGGCAGCTGACA CGAATGTAGA	<u>486</u>	SARS-Cov Replicase 1A
PMV_00029	TCACTTGCTTCCGTTGAGGGAATGGCGATGTAGT GGCTATTGA	<u>487</u>	SARS-Cov Replicase 1A
PMV_00030	GGTTTCGGATGTTACAGCGTTAATGCCGGCATCC AAACATAAT	<u>488</u>	SARS-Cov Replicase 1A
PMV_00031	TCACTTGCTTCCGTTGAGGTAGCCAGCGTGGTGG TTCATACAA	<u>489</u>	SARS-Cov Replicase 1A
PMV_00032	GGTTTCGGATGTTACAGCGTCTCCCGGCAGAAAG CTGTAAGCT	<u>490</u>	SARS-Cov Replicase 1A
PMV_00033	TCACTTGCTTCCGTTGAGGTATAGAGCCCGTGCT GGTGATGC	<u>491</u>	SARS-Cov Replicase 1A
PMV_00034	GGTTTCGGATGTTACAGCGTATCGCCATTCAAGT CTGGGAAGAA	<u>492</u>	SARS-Cov Replicase 1A
PMV_00035	TCACTTGCTTCCGTTGAGGTGGCTCAGGCCATAC TGGCATTAC	<u>493</u>	SARS-Cov Replicase 1A
PMV_00036	GGTTTCGGATGTTACAGCGTTTTGCGCCAGCGAT AGTGACTTG	<u>494</u>	SARS-Cov Replicase 1A
PMV_00037	TCACTTGCTTCCGTTGAGGTTCCTCGTCAGGCAAA GTTGAAGG	<u>495</u>	SARS-Cov Replicase 1A
PMV_00038	GGTTTCGGATGTTACAGCGTGACGGCAATTCCTG TTTGAGCAGA	<u>496</u>	SARS-Cov Replicase 1A
PMV_00074	AGCCGCTTGTCACAATGCCAATT	<u>497</u>	SARS-Cov Replicase 1A
PMV_00075	CATCACCAAGCTCGCCAACAGTT	<u>498</u>	SARS-Cov Replicase 1A
PMV_00076	AGGTTGCCATCATTTTGGCATCTT	<u>499</u>	SARS-Cov Replicase 1A
PMV_00077	CTTTGCGCCAGCGATAGTGACTT	<u>500</u>	SARS-Cov Replicase 1A
PMV_00078	ATGGCACCCGTTTCTGCAATGG	<u>501</u>	SARS-Cov Replicase 1A
PMV_00079	TCGGGCAGCTGACACGAATGTAGA	<u>502</u>	SARS-Cov Replicase 1A
PMV_00080	GAATGGCGATGTAGTGGCTATTGA	<u>503</u>	SARS-Cov Replicase 1A

id	sequence (5'-3')	SEQ ID NO:	region
PMV_00081	TAATGCCGGCATCCAAACATAAT	<u>504</u>	SARS-Cov Replicase 1A
PMV_00082	TAGCCAGCGTGGTGGTTCATACAA	<u>505</u>	SARS-Cov Replicase 1A
PMV_00083	CTCCCGGCAGAAAGCTGTAAGCT	<u>506</u>	SARS-Cov Replicase 1A
PMV_00084	TATAGAGCCCGTGCTGGTGATGC	<u>507</u>	SARS-Cov Replicase 1A
PMV_00085	ATCGCCATTCAAGTCTGGGAAGAA	<u>508</u>	SARS-Cov Replicase 1A
PMV_00086	TGGCTCAGGCCATACTGGCATTAC	<u>509</u>	SARS-Cov Replicase 1A
PMV_00087	TTTGCGCCAGCGATAGTGACTTG	<u>510</u>	SARS-Cov Replicase 1A
PMV_00088	TTCCCGTCAGGCAAAGTTGAAGG	<u>511</u>	SARS-Cov Replicase 1A
PMV_00089	GACGGCAATTCTGTGTTGAGCAGA	<u>512</u>	SARS-Cov Replicase 1A
PMV_00003	TCACTTGCTTCCGTTGAGGATGAATTACCAAGTC AATGGTTAC	<u>513</u>	SARS-Cov Replicase 1B
PMV_00004	GGTTTCGGATGTTACAGCGTATAACCAGTCGGTA CAGCTAC	<u>514</u>	SARS-Cov Replicase 1B
PMV_00005	TCACTTGCTTCCGTTGAGGGAAGCTATTTCGTCAC GTTTCG	<u>515</u>	SARS-Cov Replicase 1B
PMV_00006	GGTTTCGGATGTTACAGCGTCTGTAGAAAATCCT AGCTGGAG	<u>516</u>	SARS-Cov Replicase 1B
PMV_00007	TCACTTGCTTCCGTTGAGGCCTCTCTTGTTCTTG CTCGCA	<u>517</u>	SARS-Cov Replicase 1B
PMV_00008	GGTTTCGGATGTTACAGCGTGTGAGCCGCCACAC ATG	<u>518</u>	SARS-Cov Replicase 1B
PMV_00009	TCACTTGCTTCCGTTGAGGCTAACATGCTTAGGA TAATGG	<u>519</u>	SARS-Cov Replicase 1B
PMV_00010	GGTTTCGGATGTTACAGCGTCAGGTAAGCGTAAA ACTCATC	<u>520</u>	SARS-Cov Replicase 1B
PMV_00011	TCACTTGCTTCCGTTGAGGGCCTCTCTTGTTCTT GCTCGC	<u>521</u>	SARS-Cov Replicase 1B

id	sequence (5'-3')	SEQ ID NO:	region
PMV_00013	TCACTTGCTTCCGTTGAGGCACCGTTTCTACAGG TTAGCTAACGA	<u>522</u>	SARS-Cov Replicase 1B
PMV_00014	GGTTTCGGATGTTACAGCGTAAATGTTTACGCAG GTAAGCGTAAAA	<u>523</u>	SARS-Cov Replicase 1B
PMV_00015	TCACTTGCTTCCGTTGAGGTACACACCTCAGCGT TG	<u>524</u>	SARS-Cov Replicase 1B
PMV_00016	GGTTTCGGATGTTACAGCGTCACGAACGTGACGA AT	<u>525</u>	SARS-Cov Replicase 1B
PMV_00017	TCACTTGCTTCCGTTGAGGGCTTAGGATAATGGC CTCTC	<u>526</u>	SARS-Cov Replicase 1B
PMV_00018	GGTTTCGGATGTTACAGCGTCCACGAATTCATGA TCAACATCCC	<u>527</u>	SARS-Cov Replicase 1B
PMV_00019	TCACTTGCTTCCGTTGAGGGCTCGCAAACATAAC ACTTGC	<u>528</u>	SARS-Cov Replicase 1B
PMV_00020	GGTTTCGGATGTTACAGCGTGAGACACTCATAGA GCCTGTG	<u>529</u>	SARS-Cov Replicase 1B
PMV_00055	ATGAATTACCAAGTCAATGGTTAC	<u>530</u>	SARS-Cov Replicase 1B
PMV_00056	ATAACCAGTCGGTACAGCTAC	<u>531</u>	SARS-Cov Replicase 1B
PMV_00057	GAAGCTATTCGTCACGTTTCG	<u>532</u>	SARS-Cov Replicase 1B
PMV_00058	CTGTAGAAAAATCCTAGCTGGAG	<u>533</u>	SARS-Cov Replicase 1B
PMV_00059	CCTCTCTTGTTCTTGCTCGCA	<u>534</u>	SARS-Cov Replicase 1B
PMV_00060	GTGAGCCGCCACACATG	<u>535</u>	SARS-Cov Replicase 1B
PMV_00061	CTAACATGCTTAGGATAATGG	<u>536</u>	SARS-Cov Replicase 1B
PMV_00062	CAGGTAAGCGTAAAACTCATC	<u>537</u>	SARS-Cov Replicase 1B
PMV_00063	GCCTCTCTTGTTCTTGCTCGC	<u>538</u>	SARS-Cov Replicase 1B
PMV_00064	CACCGTTTCTACAGGTTAGCTAACGA	<u>539</u>	SARS-Cov Replicase 1B



id	sequence(5'-3')	SEQ ID NO:	region
PMV_00065	AAATGTTTACGCAGGTAAGCGTAAAA	<u>540</u>	SARS-Cov Replicase 1B
PMV_00066	TACACACCTCAGCGTTG	<u>541</u>	SARS-Cov Replicase 1B
PMV_00067	CACGAACGTGACGAAT	<u>542</u>	SARS-Cov Replicase 1B
PMV_00068	GCTTAGGATAATGGCCTCTC	<u>543</u>	SARS-Cov Replicase 1B
PMV_00069	CCACGAATTCATGATCAACATCCC	<u>544</u>	SARS-Cov Replicase 1B
PMV_00070	GCTCGCAAACATAACACTTGC	<u>545</u>	SARS-Cov Replicase 1B
PMV_00071	GAGACACTCATAGAGCCTGTG	<u>546</u>	SARS-Cov Replicase 1B
PMSL_00003	CCAGCTCCAATAGGAATGTCGCACTC	<u>547</u>	SARS-Cov Spike glycoprotein gene
PMSL_00004	TCCGCAGATGTACATATTACAATCTACG	<u>548</u>	SARS-Cov Spike glycoprotein gene
PMSU_00005	TTAAATGCACCGGCCACGGTTTG	<u>549</u>	SARS-Cov Spike glycoprotein gene
PMV_000100	ATAGCGCCAGGACAACTGGTGTT	<u>550</u>	SARS-Cov Spike glycoprotein gene
PMV_000101	TATATGCGCCAAGCTGGTGTGAGT	<u>551</u>	SARS-Cov Spike glycoprotein gene
PMV_000102	CGAGGCGGAGGTACAAATTGACAG	<u>552</u>	SARS-Cov Spike glycoprotein gene
PMV_000103	ATGAAGCCGAGCCAAACATACCAA	<u>553</u>	SARS-Cov Spike glycoprotein gene
PMV_00045	TCACTTGCTTCCGTTGAGGATGCACCGGCCACGG TTTGTG	<u>554</u>	SARS-Cov Spike glycoprotein gene
PMV_00046	GGTTTCGGATGTTACAGCGTATGCGCCAAGCTGG TGTGAGTTGA	<u>555</u>	SARS-Cov Spike glycoprotein gene
PMV_00047	TCACTTGCTTCCGTTGAGGTGCTGGCGCTGCTCT TCAAATACC	<u>556</u>	SARS-Cov Spike glycoprotein gene
PMV_00048	GGTTTCGGATGTTACAGCGTCGGGGCTGCTTGTG GGAAGG	<u>557</u>	SARS-Cov Spike glycoprotein gene

id	sequence (5'-3')	SEQ ID NO:	region
PMV_00049	TCACTTGCTTCCGTTGAGGATAGCGCCAGGACAA ACTGGTGTT	<u>558</u>	SARS-Cov Spike glycoprotein gene
PMV_00050	GGTTTCGGATGTTACAGCGTTATATGCGCCAAGC TGGTGTGAGT	<u>559</u>	SARS-Cov Spike glycoprotein gene
PMV_00051	TCACTTGCTTCCGTTGAGGCGAGGCGGAGGTACA AATTGACAG	<u>560</u>	SARS-Cov Spike glycoprotein gene
PMV_00052	GGTTTCGGATGTTACAGCGTATGAAGCCGAGCCA AACATACCAA	<u>561</u>	SARS-Cov Spike glycoprotein gene
PMV_00096	ATGCACCGGCCACGGTTTGTG	<u>562</u>	SARS-Cov Spike glycoprotein gene
PMV_00097	ATGCGCCAAGCTGGTGTGAGTTGA	<u>563</u>	SARS-Cov Spike glycoprotein gene
PMV_00098	TGCTGGCGCTGCTCTTCAAATACC	<u>564</u>	SARS-Cov Spike glycoprotein gene
PMV_00099	CGGGGCTGCTTGTGGGAAGG	<u>565</u>	SARS-Cov Spike glycoprotein gene

Please replace Table 19, beginning on page 54 and bridging to page 61, with a new Table 19 as follows:

Table 19. Exemplary primers for non-SARS-CoV infectious organism causing SARS-like symptoms

id	Sequence (5' - 3')	SEQ ID NO:	species
PMIA_00001	TTGTGCGACAATGCTTCA	<u>566</u>	Influenza A virus
PMIA_00002	GACATTTGAGAAAGCTTGCC	<u>567</u>	Influenza A virus
PMIA_00003	AGGGACAACCTNGAACCTGG	<u>568</u>	Influenza A virus
PMIA_00004	AGGAGTTGAACCAAGACGCATT	<u>569</u>	Influenza A virus
PMIA_00005	ACCACATTCCCTTATACTGGAG	<u>570</u>	Influenza A virus
PMIA_00006	TTAGTCATCATCTTTCTCACAACA	<u>571</u>	Influenza A virus
PMIA_00007	ACAAATTGCTTCAAATGAGAAC	<u>572</u>	Influenza A virus
PMIA_00008	TGTCTCCGAAGAAATAAGATCC	<u>573</u>	Influenza A virus
PMIA_00009	GCGCAGAGACTTGAAGATGT	<u>574</u>	Influenza A virus
PMIA_00010	CCTTCCGTAGAAGGCCCT	<u>575</u>	Influenza A virus

id	Sequence (5' - 3')	SEQ ID NO:	species
PMIB_00001	CACAATGGCAGAATTTAGTGA	<u>576</u>	Influenza B virus
PMIB_00002	GTCAGTTTGATCCCGTAGTG	<u>577</u>	Influenza B virus
PMIB_00003	CAGATCCCAGAGTGGACTCA	<u>578</u>	Influenza B virus
PMIB_00004	TGTATTACCCAAGGGTTGTTAC	<u>579</u>	Influenza B virus
PMIB_00005	GATCAGCATGACAGTAACAGGA	<u>580</u>	Influenza B virus
PMIB_00006	ATGTTCGGTAAAAGTCGTTTAT	<u>581</u>	Influenza B virus
PMIB_00007	CCACAGGGGAGATTCCAAAG	<u>582</u>	Influenza B virus
PMIB_00008	GACATTCTTCCTGATTGATAATC	<u>583</u>	Influenza B virus
PMIB_00009	CAAACAACGGTAGACCAATATA	<u>584</u>	Influenza B virus
PMIB_00010	AGGTTTCAGTATCTATCACAGTCTT	<u>585</u>	Influenza B virus
PMIB_00011	ATGTCCAACATGGATATTGAC	<u>586</u>	Influenza B virus
PMIB_00012	GCTCTTCCTATAAATCGAATG	<u>587</u>	Influenza B virus
PMIB_00013	TGATCAAGTGATCGGAAGTAG	<u>588</u>	Influenza B virus
PMIB_00014	GATGGTCTGCTTAATTGGAA	<u>589</u>	Influenza B virus
PMIB_00015	ACAGAAGATGGAGAAGGCAA	<u>590</u>	Influenza B virus
PMIB_00016	ATTGTTTCTTTGGCCTGGAT	<u>591</u>	Influenza B virus
PMAd1_00001	TGGCGGTATAGGGGTAAGT	<u>592</u>	Human adenovirus
PMAd1_00002	ATTGCGGTGATGGTTAAAGG	<u>593</u>	Human adenovirus
PMAd1_00003	TTTGCCGATCCCACTTATC	<u>594</u>	Human adenovirus
PMAd1_00004	GCAAGTCTACCACGGCATT	<u>595</u>	Human adenovirus
PMAd2_00001	CTCCGTTATCGCTCCATGTT	<u>596</u>	Human adenovirus
PMAd2_00002	AAGGACTGGTCGTTGGTGTC	<u>597</u>	Human adenovirus
PMAd2_00003	AAATGCCGTGGTAGATTGTC	<u>598</u>	Human adenovirus
PMAd2_00004	GTTGAAGGGTTGACGTTGT	<u>599</u>	Human adenovirus
PMAd3_00001	TCCTCTGGATGGCATAGGAC	<u>600</u>	Human adenovirus
PMAd3_00002	TGTTGGTGTTAGTGGGCAAA	<u>601</u>	Human adenovirus

id	Sequence (5' - 3')	SEQ ID NO:	species
PMAd3_00003	ACATGGTCCTGCAAAGTTCC	602	Human adenovirus
PMAd3_00004	GCATTGTGCCACGTTGTATC	603	Human adenovirus
PMAd4_00001	CGCTTCGGAGTACCTCAGTC	604	Human adenovirus
PMAd4_00002	CTGCATCATTGGTGTCAACC	605	Human adenovirus
PMAd4_00003	GGCACCTTTTACCTCAACCA	606	Human adenovirus
PMAd4_00004	TCTGGACCAAGAACCAGTCC	607	Human adenovirus
PMAd5_00001	GGCCTACCCTGCTAACTTCC	608	Human adenovirus
PMAd5_00002	ATAAAGAAGGGTGGGCTCGT	609	Human adenovirus
PMAd5_00003	ATCGCAGTTGAATGCTGTTG	610	Human adenovirus
PMAd5_00004	GTTGAAGGGGTGACGTTGT	611	Human adenovirus
PMAd7_00001	ACATGGTCCTGCAAAGTTCC	612	Human adenovirus
PMAd7_00002	GATCGAACCCTGATCCAAGA	613	Human adenovirus
PMAd7_00003	AACACCAACCGAAGGAGATG	614	Human adenovirus
PMAd7_00004	CCTATGCCATCCAGAGGAAA	615	Human adenovirus
PMAd11_00001	CAGATGCTCGCCAACTACAA	616	Human adenovirus
PMAd11_00002	AGCCATGTAACCCACAAAGC	617	Human adenovirus
PMAd11_00003	ACGGACGTTATGTGCCTTTC	618	Human adenovirus
PMAd11_00004	GGGAATATTGGTTGCATTGG	619	Human adenovirus
PMAd21_00001	ACTGGTTCCTGGTCCAGATG	620	Human adenovirus
PMAd21_00002	AGCCATGTAACCCACAAAGC	621	Human adenovirus
PMAd21_00003	CTGGATATGGCCAGCACTTT	622	Human adenovirus
PMAd21_00004	CACCTGAGGTTCTGGTTGGT	623	Human adenovirus
PMAd23_00001	TAATGAAAAGGGCGGACAAG	624	Human adenovirus
PMAd23_00002	GCCAATGTAGTTTGGCCTGT	625	Human adenovirus
PMAd23_00003	AACTCCGCGGTAGACAGCTA	626	Human adenovirus
PMAd23_00004	CGTAGGTGTTGGTGTGGTG	627	Human adenovirus

id	Sequence (5' - 3')	SEQ ID NO:	species
PMV_a0061	TCACTTGCTTCCGTTGAGGTTGGGGTGATGG GTTTCAGATTAA	<u>628</u>	HCoV-OC43
PMV_a0062	GGTTTCGGATGTTACAGCGTCTCGGGAAGAT CGCCTTCTTCTA	<u>629</u>	HCoV-OC43
PMV_b0061	TTGGGGTGATGGGTTTCAGATTAA	<u>630</u>	HCoV-OC43
PMV_b0062	CTCGGGAAGATCGCCTTCTTCTA	<u>631</u>	HCoV-OC43
PMV_a0053	TCACTTGCTTCCGTTGAGGTTGGGCTGGCGG TTTAGAGTTGA	<u>632</u>	HCoV-229E
PMV_a0054	GGTTTCGGATGTTACAGCGTGTGCGACCGCC CTTGTTTATGG	<u>633</u>	HCoV-229E
PMV_a0055	TCACTTGCTTCCGTTGAGGGCGTTGTTGGCC TTTTTCTTGCT	<u>634</u>	HCoV-229E
PMV_a0056	GGTTTCGGATGTTACAGCGTGCCCGGCATTA TTTCATTGTTCTG	<u>635</u>	HCoV-229E
PMV_a0057	TCACTTGCTTCCGTTGAGGACAAAAGCCGCT GGTGGTAAAG	<u>636</u>	HCoV-229E
PMV_a0058	GGTTTCGGATGTTACAGCGTCAGAAATCATA ACGGGCAAACCTCA	<u>637</u>	HCoV-229E
PMV_a0059	TCACTTGCTTCCGTTGAGGAAGAGTTATTGC TGGCGTTGTTGG	<u>638</u>	HCoV-229E
PMV_a0060	GGTTTCGGATGTTACAGCGTGCCCGGCATTA TTTCATTGTTCTG	<u>639</u>	HCoV-229E
PMV_b0053	TTGGGCTGGCGGTTTAGAGTTGA	<u>640</u>	HCoV-229E
PMV_b0054	GTGCGACCGCCCTTGTTTATGG	<u>641</u>	HCoV-229E
PMV_b0055	GCGTTGTTGGCCTTTTCTTGCT	<u>642</u>	HCoV-229E
PMV_b0056	GCCCCGCATTATTTTCATTGTTCTG	<u>643</u>	HCoV-229E
PMV_b0057	ACAAAAGCCGCTGGTGGTAAAG	<u>644</u>	HCoV-229E
PMV_b0058	CAGAAATCATAACGGGCAAACCTCA	<u>645</u>	HCoV-229E
PMV_b0059	AAGAGTTATTGCTGGCGTTGTTGG	<u>646</u>	HCoV-229E
PMV_b0060	GCCCCGCATTATTTTCATTGTTCTG	<u>647</u>	HCoV-229E
PMHE_00001	GGTGGTAACCCCTCGCAGGA	<u>648</u>	Human enteric coronaviruse

id	Sequence (5' - 3')	SEQ ID NO:	species
PMHE_00002	TGGCTCTTCCCTTTGGGCACT	<u>649</u>	Human enteric coronaviruse
PMHE_00003	GAGAATGAACCTTATGTCGGCACCTG	<u>650</u>	Human enteric coronaviruse
PMHE_00004	TTCCGCAAGTCTTCACTTTCTCCAA	<u>651</u>	Human enteric coronaviruse
PMHE_00005	CAGCTTTCAGCCAGGGACGTGT	<u>652</u>	Human enteric coronaviruse
PMHE_00006	TTTCCAGCTTTTGCGCAGTGGT	<u>653</u>	Human enteric coronaviruse
PMHE_00007	TCTGTTTTGGTGCAGGTCAATTTGTG	<u>654</u>	Human enteric coronaviruse
PMHE_00008	ATGAACCAGGTCGTAAGCATCCTCAA	<u>655</u>	Human enteric coronaviruse
PMHE_00009	GTTGCTTGTC AACCCCCG TACTGTTA	<u>656</u>	Human enteric coronaviruse
PMHE_00010	AGGACACCTGCCATAGGGGTAGAGAG	<u>657</u>	Human enteric coronaviruse
PMHE_00011	GGTTGTTGACTCGCGGTGGA	<u>658</u>	Human enteric coronaviruse
PMHE_00012	GGGGTAGAGAGGCCAAACACTGC	<u>659</u>	Human enteric coronaviruse
PMRh_00001	ACATGGTCCCATTGGATTGT	<u>660</u>	Human rhinovirus
PMRh_00002	TGAGGAAATCTTTCGCCACT	<u>661</u>	Human rhinovirus
PMRh_00003	ATGTTGCCCCCTAGTCTGTG	<u>662</u>	Human rhinovirus
PMRh_00004	TTCTGAAGGTGGTGTGTTGC	<u>663</u>	Human rhinovirus
PMRh_00005	TGGTATTCATGTTGGCGGTA	<u>664</u>	Human rhinovirus
PMRh_00006	ACAGCAGGTTCTTGTCACC	<u>665</u>	Human rhinovirus
PMRh_00007	TCTTGCCTCCAATGGCTAGT	<u>666</u>	Human rhinovirus
PMRh_00008	TGACATGCCTGCATTGAGTT	<u>667</u>	Human rhinovirus
PMRh_00009	TCCCAATATGCCCTCTTCAG	<u>668</u>	Human rhinovirus
PMRh_00010	CGCTGATGGGGATTGAGTAT	<u>669</u>	Human rhinovirus

id	Sequence (5' - 3')	SEQ ID NO:	species
PMRh_00011	TGTGCTCAGTGTGCTTCCTC	<u>670</u>	Human rhinovirus
PMRh_00012	TGCACCCATGATGACAATCT	<u>671</u>	Human rhinovirus
PMRh_00013	GCAGTTCTTGCCAAAGAAGG	<u>672</u>	Human rhinovirus
PMRh_00014	TGAAGGGTTTTTGGTCCATC	<u>673</u>	Human rhinovirus
PMRh_00015	TGCCTGATGCCCTTAAAAAC	<u>674</u>	Human rhinovirus
PMRh_00016	GGGTGTGATTGTACCCGACT	<u>675</u>	Human rhinovirus
PMMP_00001	CTTAACAGTTGTATGCATTGGAAACT	<u>676</u>	Mycoplasma pneumoniae
PMMP_00002	GTTTACGGTGTGGACTACTAGGGTAT	<u>677</u>	Mycoplasma pneumoniae
PMMP_00003	CTATGCTGAGAAGTAGAATAGCCACA	<u>678</u>	Mycoplasma pneumoniae
PMMP_00004	TGGTACAGTCAAACCTAGCCATTAC	<u>679</u>	Mycoplasma pneumoniae
PMMP_00005	ATACCCTAGTAGTCCACACCGTAAAC	<u>680</u>	Mycoplasma pneumoniae
PMMP_00006	ATGTCAAGTCTAGGTAAGGTTTTTCG	<u>681</u>	Mycoplasma pneumoniae
PMMP_00007	AGGCGAAAACCTTAGGCCATT	<u>682</u>	Mycoplasma pneumoniae
PMMP_00008	CCGTCAATTCGTTTGAGTT	<u>683</u>	Mycoplasma pneumoniae
PMMP_00009	CGACGGTACACGAAAAACCT	<u>684</u>	Mycoplasma pneumoniae
PMMP_00010	TCCCTTCCTTCCTCCAATTT	<u>685</u>	Mycoplasma pneumoniae
PMR_00001	ATTCCCATGGAGAACTCCTAGAT	<u>686</u>	Rubella virus
PMR_00002	GTGATCACTGACCTGCATCTG	<u>687</u>	Rubella virus
PMR_00003	GTAAGAGACCACGTCCGATCAAT	<u>688</u>	Rubella virus
PMR_00004	GAGGACGTGTAGGGCTTCTTTAG	<u>689</u>	Rubella virus
PMR_00005	ATCGGACCTCGCTTAGGACT	<u>690</u>	Rubella virus
PMR_00006	CTGGGTATCACGGCTACGAT	<u>691</u>	Rubella virus

id	Sequence (5' - 3')	SEQ ID NO:	species
PMR_00007	AGAGACCACGTCCGATCAAT	<u>692</u>	Rubella virus
PMR_00008	TGAGGACGTGTAGGGCTTCT	<u>693</u>	Rubella virus
PMR_00009	GTCAACGCCTACTCCTCTGG	<u>694</u>	Rubella virus
PMR_00010	GTCTTGTGAGGGTGCTGGAC	<u>695</u>	Rubella virus
PMM_00001	CACATTGGCATCTGAACTCG	<u>696</u>	Measles virus
PMM_00002	TCTGTTTGACCCTCCTGTCC	<u>697</u>	Measles virus
PMM_00003	AGATTGCAATGCATACTACTGAGGAC	<u>698</u>	Measles virus
PMM_00004	ATGCAGTGTCAATGTCTAGAGGTGT	<u>699</u>	Measles virus
PMM_00005	CAATGCATACTACTGAGGACAGGA	<u>700</u>	Measles virus
PMM_00006	ATGCAGTGTCAATGTCTAGAGGTG	<u>701</u>	Measles virus
PMM_00007	TACCATCAGAGGTCAATTCTCAA	<u>702</u>	Measles virus
PMM_00008	CTACTTCAAACACTCGGTACATGC	<u>703</u>	Measles virus
PMM_00009	CATGTCGCTGTCTCTGTTAGACTT	<u>704</u>	Measles virus
PMM_00010	CAAGCCTGGATTTCTTATAACACC	<u>705</u>	Measles virus
PMRSV_00001	AAACCAAAGAAGAAACCAACCAT	<u>706</u>	Human respiratory syncytial virus
PMRSV_00002	TGTTCTAATGTGGTTGTGTCGAG	<u>707</u>	Human respiratory syncytial virus
PMRSV_00003	TGCTAAAAGAGATGGGAGAAGTG	<u>708</u>	Human respiratory syncytial virus
PMRSV_00004	ATCCTTTGGTATGAGACCCTTGT	<u>709</u>	Human respiratory syncytial virus
PMRSV_00005	ACAAGGGTCTCATACCAAAGGAT	<u>710</u>	Human respiratory syncytial virus
PMRSV_00006	GCTAAAACTCCCCATCTTAGCAT	<u>711</u>	Human respiratory syncytial virus
PMRSV_00007	TTTATGATGCAGCCAAAGCA	<u>712</u>	Human respiratory syncytial virus
PMRSV_00008	TCCATGAAATTCAGGTGCAA	<u>713</u>	Human respiratory syncytial virus



id	Sequence (5' - 3')	SEQ ID NO:	species
PMRSV_00009	AAAAACACCAGCCAAAACGA	<u>714</u>	Human respiratory syncytial virus
PMRSV_00010	CTGTGGGTGTTTGTGTGGAG	<u>715</u>	Human respiratory syncytial virus
PMRSV_00011	CCAAAGCATATGCAGAGCAA	<u>716</u>	Human respiratory syncytial virus
PMRSV_00012	TCCATGAAATTCAGGTGCAA	<u>717</u>	Human respiratory syncytial virus
PMPI_00001	GCATGGAAACTAGCAGCACA	<u>718</u>	Parainfluenza
PMPI_00002	GGTGTGTGGTCTTCGAGGT	<u>719</u>	Parainfluenza
PMPI_00003	GGCTCCATAGTATCATCGACAAC	<u>720</u>	Parainfluenza
PMPI_00004	CCTAGAGGCCCTGTGTATACCTT	<u>721</u>	Parainfluenza
PMPI_00005	ACACAACAAACAATGCAAACAAC	<u>722</u>	Parainfluenza
PMPI_00006	TTAACATGCGCTTAGCAAATACA	<u>723</u>	Parainfluenza
PMPI_00007	TTAGCTCACTCATTGGACACAGA	<u>724</u>	Parainfluenza
PMPI_00008	GTCTCTCGTTTTGACAATGAACC	<u>725</u>	Parainfluenza
PMPI_00009	TCTCACTACAAACGGTGTCAATG	<u>726</u>	Parainfluenza
PMPI_00010	TCTAGATCCGCATTCTCTCTTTG	<u>727</u>	Parainfluenza
PMPI_00011	ACAGATGGGTTTCATTGTCAAAC	<u>728</u>	Parainfluenza
PMPI_00012	GCTTTGACCAACACTATCCAAAC	<u>729</u>	Parainfluenza
PMPI_00013	GCTGAACACCCAGATTTACAAAG	<u>730</u>	Parainfluenza
PMPI_00014	ACAGCTCTCCATTTTCATGGTTTA	<u>731</u>	Parainfluenza
PMPI_00015	ATATGCATTTGTCAATGGAGGAG	<u>732</u>	Parainfluenza
PMPI_00016	CATTTGGTGTGTAAAATGCAAGA	<u>733</u>	Parainfluenza
PMPI_00017	CACAGAACACCAGAACAACAAGA	<u>734</u>	Parainfluenza
PMPI_00018	TTGGGACTGTTAACCAATACACC	<u>735</u>	Parainfluenza
PMME_00001	CATCCCAAAAATTGCCAGAT	<u>736</u>	Human metapneumovirus

id	Sequence (5' - 3')	SEQ ID NO:	species
PMME_00002	TTTGGGCTTTGCCTTAAATG	<u>737</u>	Human metapneumovirus
PMME_00003	ACACCCTCATCATTGCAACA	<u>738</u>	Human metapneumovirus
PMME_00004	GCCCTTCTGACTGTGGTCTC	<u>739</u>	Human metapneumovirus
PMME_00005	CGACACAGCAGCAGGAATTA	<u>740</u>	Human metapneumovirus
PMME_00006	TCAAAGCTGCTTGACACTGG	<u>741</u>	Human metapneumovirus

Please replace Table 20, beginning on page 61 and bridging to page 66, with a new Table 20 as follows:

Table 20. Exemplary primers for non-SARS-CoV infectious organism damaging the subject's immune system

id	sequence (5' - 3')	SEQ. ID NO:	species
PMTTV_00001	TGGGGCCAGACTTCGCCATA	<u>742</u>	TTV
PMTTV_00002	AGCTTCCGCCGAGGATGACC	<u>743</u>	TTV
PMTTV_00003	CTTGGGGGCTCAACGCCTTC	<u>744</u>	TTV
PMTTV_00004	GCGAAGTCTGGCCCCACTCA	<u>745</u>	TTV
PMTTV_00005	CCACAGGCCAACCGAATGCT	<u>746</u>	TTV
PMTTV_00006	AGCCCGAATTGCCCTTGAC	<u>747</u>	TTV
PMTTV_00007	AGCGAATCCTGGGAGTCAAACCTCAG	<u>748</u>	TTV
PMTTV_00008	GGCCTCGTACTCCTCTTTCCAGTCA	<u>749</u>	TTV
PMTTV_00009	GCCCCTTTGCATACCACTCAGACAT	<u>750</u>	TTV
PMTTV_00010	TGGAATGTGAGTTCCGGTGAGTTGT	<u>751</u>	TTV
PMTTV_00011	TGTCAGTAACAGGGGTCGCCATAGA	<u>752</u>	TTV
PMTTV_00012	TGTGACGTATGGACGACCTTTGACC	<u>753</u>	TTV
PMV_11047	CACAGACAGAGGAGAAGGCAAC	<u>754</u>	TTV
PMV_11048	AATAGGCACATTACTACTACCTCCTG	<u>755</u>	TTV

id	sequence (5' - 3')	SEQ ID NO:	species
PMTP_00001	GCGGTCGGTAGGAGGATAAAGGAAA	<u>756</u>	TP
PMTP_00002	CCGGGGATTGTGTCTACAGGGTTTCT	<u>757</u>	TP
PMTP_00003	CAGACGCTCATCCAACCTCTGAGAA	<u>758</u>	TP
PMTP_00004	CCGTTGTACCGTCTTTTTGGACGTT	<u>759</u>	TP
PMTP_00005	CACGCTCTACCTCATTCGAGAGCAA	<u>760</u>	TP
PMTP_00006	GTTGTGTTGCAACGAACACGCTACA	<u>761</u>	TP
PMTP_00007	AGCGGTCGGTAGGAGGATAAAGGAA	<u>762</u>	TP
PMTP_00008	ACCGGGGATTGTGTCTACAGGGTTTC	<u>763</u>	TP
PMV_11025	AACACGATCCGCTACGACTACTAC	<u>764</u>	TP
PMV_11026	CCCTATACCCGTTGCAATCAAAG	<u>765</u>	TP
PMHIV1_00001	ATGGGCGCAGCCTCAATGAC	<u>766</u>	HIV1
PMHIV1_00002	CCCCAAATCCCCAGGAGCTG	<u>767</u>	HIV1
PMHIV1_00003	GGGACAGCTACAACCATCCCTTCAG	<u>768</u>	HIV1
PMHIV1_00004	GACCTGATTGCTGTGTCTGTGTCA	<u>769</u>	HIV1
PMHIV1_00005	GGGATGGAAAGGATCACCAGCAATA	<u>770</u>	HIV1
PMHIV1_00006	GTCTGGTGTGGTAAGTCCCCACCTC	<u>771</u>	HIV1
PMHIV1_00007	AAGGATCAACAGCTCCTGGGGATT	<u>772</u>	HIV1
PMHIV1_00008	TTCTTGCTGGTTTTGCGATTCTTCA	<u>773</u>	HIV1
PMV_11055	TAATCCACCTATCCCAGTAGGAGAAAT	<u>774</u>	HIV1
PMV_11056	GGTCCTTGCTTTATGTCCAGAATGC	<u>775</u>	HIV1
PMV_11057	TGGGAAGTTCAATTAGGAATACCAC	<u>776</u>	HIV1
PMV_11058	TCCTACATACAAATCATCCATGTATTG	<u>777</u>	HIV1
PMHGV_00001	GCCGGCGATGACTGCTTGAT	<u>778</u>	HGV
PMHGV_00002	TCCGGAAGTCCGTGGTCAGG	<u>779</u>	HGV
PMHGV_00003	ACGGTGGGAGTCGCGTTGAC	<u>780</u>	HGV
PMHGV_00004	GGCCACGCAAACCAACAAGG	<u>781</u>	HGV

id	sequence (5' - 3')	SEQ ID NO:	species
PMHGV_00005	CGGCCAAAAGGTGGTGGATG	<u>782</u>	HGV
PMHGV_00006	CGGGCTCGGTTTAACGACGA	<u>783</u>	HGV
PMHGV_00007	GCCACGGGCAAAATCAGTGG	<u>784</u>	HGV
PMHGV_00008	TGTCGCGATCCGATGATCCA	<u>785</u>	HGV
PMHGV_00009	CGCGTGTGAGCTAAAGTGGGAAAAGT	<u>786</u>	HGV
PMHGV_00010	ATCGTCACCAACAGGAAGACCATGA	<u>787</u>	HGV
PMHGV_00011	TCGCTCTCGGGTTGGTTTTGTATTC	<u>788</u>	HGV
PMHGV_00012	CATCCACCTTAGGCTCCCTGTTGAC	<u>789</u>	HGV
PMV_11045	GGGTTGGTAGGTCTGTAATCCC	<u>790</u>	HGV
PMV_11046	GTACGTGGGCGTCGTTTGC	<u>791</u>	HGV
PMV_11001	CCTTTCCACCATCCAGCAGT	<u>792</u>	HEV
PMV_11002	CGAGCTTTACCCACCTTCAGC	<u>793</u>	HEV
PMHEV_00001	CTGGCGGTGGGCTCTGTCTAT	<u>794</u>	HEV
PMHEV_00002	ACCGAGGCGGGAGCAAGTCT	<u>795</u>	HEV
PMHEV_00003	ACGGGCGGATCGATTGTGAG	<u>796</u>	HEV
PMHEV_00004	GGCAGCGACATAGCGCACCT	<u>797</u>	HEV
PMHEV_00005	AGCTCACCACCACGGCTGCT	<u>798</u>	HEV
PMHEV_00006	CTGAGACGACGGGGCGAGAG	<u>799</u>	HEV
PMHEV_00007	ATCGCGCCCCTTTTCTGTCC	<u>800</u>	HEV
PMHEV_00008	GGGGGCGACCATCAAGTGTG	<u>801</u>	HEV
PMHDV_00001	GACGGGCCGGCTGTTCTTCT	<u>802</u>	HDV
PMHDV_00002	GACTCCGGGCCTGGGAAGAG	<u>803</u>	HDV
PMHDV_00003	ACTCCGGCCGAAAGGTCGAG	<u>804</u>	HDV
PMHDV_00004	GGCGGAACACCCACCGACTA	<u>805</u>	HDV
PMHDV_00005	CCATGACTCTGGAGACATCCTGGAA	<u>806</u>	HDV
PMHDV_00006	CGTCAGAGCTCTCTGTTGCTGAAG	<u>807</u>	HDV

id	sequence (5' - 3')	SEQ ID NO:	species
PMHDV_00007	CCTTCTCTCGTCTTCCTCGGTCAAC	808	HDV
PMHDV_00008	CCGAACGGACCAGATGGAGATAGAC	809	HDV
PMHDV_00009	GCTCCCGAGAGGGATAAAACGGTAA	810	HDV
PMHDV_00010	GAGTGCTCTCCAACTTGGCAGTTG	811	HDV
PMHDV_00011	TCTCGTCTTCCTCGGTCAACCTCTT	812	HDV
PMHDV_00012	CCGAACGGACCAGATGGAGATAGAC	813	HDV
PMV_11041	AACATTCCGAAGGGGACCGT	814	HDV
PMV_11042	GGCATCCGAAGGAGGACG	815	HDV
PMHCV_00001	GGCGCTGGAAGAGGGTCTACTACC	816	HCV
PMHCV_00002	TGTTCAAGCTGATCCCTGGCTATGA	817	HCV
PMHCV_00003	ACATCTGGGACTGGATATGCGAGGT	818	HCV
PMHCV_00004	ATCCTCATCGTCCCGTTTTTGACAT	819	HCV
PMHCV_00005	TGTGCCAGGACCATCTTGAATTTTG	820	HCV
PMHCV_00006	AGGCGGATCAAACACTTCCACATCT	821	HCV
PMHCV_00007	GGGGTGCAAATGATACGGATGTCTT	822	HCV
PMHCV_00008	AGAGTATGTGGCTTCCGGATGCTTG	823	HCV
PMHCV_00009	ACACGCCGTGGGCCTATTCA	824	HCV
PMHCV_00010	GCCGGGACCTTGGTGCTCTT	825	HCV
PMHCV_00011	CACGCCGTGGGCCTATTCA	826	HCV
PMHCV_00012	GCCGGGACCTTGGTGCTCTT	827	HCV
PMV_11039	CTCGCAAGCACCTATCAGGCAGT	828	HCV
PMV_11040	GCAGAAAGCGTCTAGCCATGGCGT	829	HCV
PMHCMV_00001	GCGCCTGCTGCTCGAAATGT	830	HCMV
PMHCMV_00002	GTCGCGGCTGTTGCGGTAGT	831	HCMV
PMHCMV_00003	CCCCACGTCCATCTGCGTCT	832	HCMV
PMHCMV_00004	GCCCCAGCAGTCTCACCAG	833	HCMV

id	sequence (5' - 3')	SEQ ID NO:	species
PMHCMV_00005	GCTCACGCACCCTGGAGGAC	834	HCMV
PMHCMV_00006	AGTTCCAGCCCACGCACCAG	835	HCMV
PMHCMV_00007	GTGCAGTTTtaggtggcagttcatgc	836	HCMV
PMHCMV_00008	GGAAAGGGGAGGGTAGAAACGTGAG	837	HCMV
PMHCMV_00009	TGTGATTGCGTGTGCAGTTTtaggtg	838	HCMV
PMHCMV_00010	GGGGAGGGTAGAAACGTGAGTCTCC	839	HCMV
PMV_11051	ATTCCAAGCGGCCTCTGATAA	840	HCMV
PMV_11052	TCTTCCTCTGGGGCAACTTCC	841	HCMV
PMHBV_00001	TCGCAGTCCCCAACCTCCAA	842	HBV
PMHBV_00002	CAGGGTCCCGTGCTGGTTGT	843	HBV
PMHBV_00003	GCAGCCGGTCTGGAGCAAAA	844	HBV
PMHBV_00004	GCAGACGGAGAAGGGGACGA	845	HBV
PMHBV_00005	CGCCTCATTTTgCGGGTCAC	846	HBV
PMHBV_00006	TGGTTGGCTTGTGGCCAGTG	847	HBV
PMHBV_00007	ATCAAGGTATGTTGCCCCGTTGTCC	848	HBV
PMHBV_00008	AGGCCCACTCCCATAGGTATTTTGC	849	HBV
PMHBV_00009	CCTAGGACCCCTGCTCGTGTTACAG	850	HBV
PMHBV_00010	GCGATAACCAGGACAAATTGGAGGA	851	HBV
PMHBV_00011	CTGCGCACCATTATCATGCAACTTT	852	HBV
PMHBV_00012	AGTAGATCCCGGACGGAAGGAAAGA	853	HBV
PMV_11037	GTTCAAGCCTCCAAGCTGTG	854	HBV
PMV_11038	TCAGAAGGCAAAAAGAGAGTAACT	855	HBV
PMHAV_00001	GATGTTTGGGACGTCACCTT	856	HAV
PMHAV_00002	CTGGATGAGAGCCAGTCCTC	857	HAV
PMHAV_00003	ATTGCATTGGCAACCAAAAT	858	HAV
PMHAV_00004	ATCTCATTGGGCATCCTGAC	859	HAV

id	sequence (5' - 3')	SEQ. ID NO:	species
PMHAV_00005	GACTGGAGGTTGGGAAACAA	<u>860</u>	HAV
PMHAV_00006	AGCAGCCAGAGAGAATCCAA	<u>861</u>	HAV
PMHAV_00007	TAAGCATTTTTCCCGCAAAG	<u>862</u>	HAV
PMHAV_00008	AGGCATTCATGACCCATCTC	<u>863</u>	HAV
PMHAV_00009	CCAACCAAATATCATTGAGGTAGAC	<u>864</u>	HAV
PMHAV_00010	GACTTCGTGTACCTATTCACCTCGAT	<u>865</u>	HAV
PMHAV_00011	GGGTTTCCTTATGTTCAAGAAAAAT	<u>866</u>	HAV
PMHAV_00012	CCAAACTTTCTCTAATGGTCTCAA	<u>867</u>	HAV
PMV_11035	TTTTGCTCCTCTTTACCATGCTATG	<u>868</u>	HAV
PMV_11036	GGAAATGTCTCAGGTACTTTCTTTG	<u>869</u>	HAV
PMEBV_00001	AACCCAATAGCATGACAGCCAATCC	<u>870</u>	EBV
PMEBV_00002	TCAGCCCCAGAGACACGGTATATGA	<u>871</u>	EBV
PMEBV_00003	TGAACCTGGGACCTATTGATGCAGA	<u>872</u>	EBV
PMEBV_00004	CAGGGGAATCTCTGCCAACTTTGAG	<u>873</u>	EBV
PMEBV_00005	TGCACAGTGACAGTGGGAGAAACAC	<u>874</u>	EBV
PMEBV_00006	AAGAATGGAAAGGGTTGGCAGTGTG	<u>875</u>	EBV
PMEBV_00007	GTGCACAGTGACAGTGGGAGAAACA	<u>876</u>	EBV
PMEBV_00008	AAGAATGGAAAGGGTTGGCAGTGTG	<u>877</u>	EBV
PMV_11053	CCCACGCGCGCATAATG	<u>878</u>	EBV
PMV_11054	TTCACTTCGGTCTCCCTTAG	<u>879</u>	EBV
PMB19_00001	TGGGCCGCCAAGTACAGGAA	<u>880</u>	B19
PMB19_00002	GGGTTGCCCGCCTAAATGG	<u>881</u>	B19
PMB19_00003	CCCTATTAGTGGGGCAGCATGTGTT	<u>882</u>	B19
PMB19_00004	CCACCAAGCTTTTCCCTGCTACATC	<u>883</u>	B19
PMB19_00005	CAGTGTCACAGCCATACCACCACTG	<u>884</u>	B19
PMB19_00006	TGCTGGGTTCTTTATTGGGGAAAT	<u>885</u>	B19

id	sequence (5' - 3')	SEQ ID NO:	species
PMB19_00007	CCCATTGCATTAATGTAGGGGCTTG	<u>886</u>	B19
PMB19_00008	ATCACTTTCCACCATTGCGCACTT	<u>887</u>	B19
PMV_11049	CCTTTCCACCATCCAGCAGT	<u>888</u>	B19
PMV_11050	CGAGCTTTACCCACCTTCAGC	<u>889</u>	B19

Please replace Table 21, beginning on page 66 and bridging to page 68, with a new Table 21 as follows:

Table 21. Exemplary primers for non-SARS-CoV coronaviridae virus

seqid	sequence (5' - 3')	SEQ ID NO:
PMIBV_00001	GGAACAGGACCTGCCGCTGA	<u>890</u>
PMIBV_00002	ATCAGGTCCGCCATCCGAGA	<u>891</u>
PMIBV_00003	AAAGGTGGAAGAAAACCAGTCCCAGA	<u>892</u>
PMIBV_00004	GCCATCCGAGAATCGTAGTGGGTATT	<u>893</u>
PMMHV_00001	CAGCGCCAGCCTGCCTCTAC	<u>894</u>
PMMHV_00002	TGCTGCACTGGGCACTGCTT	<u>895</u>
PMMHV_00003	GGAAATTACCGACTGCCCTCAAACA	<u>896</u>
PMMHV_00004	TGATTATTTGGTCCACGCTCGGTTT	<u>897</u>
PMEQ_00001	TCCCGCGCATCCAGTAGAGC	<u>898</u>
PMEQ_00002	CTGCGGCTTTGTGGCATCCT	<u>899</u>
PMEQ_00003	TTTGCTGAAGGACAAGGTGTGCCTA	<u>900</u>
PMEQ_00004	CCAGAAGACTCCGTCAATGTTGGTG	<u>901</u>
PMCA_00001	AAAAACGTGGTCGTTCCAATTCTCG	<u>902</u>
PMCA_00002	CCATGCGATAGCGGCTTTGTCTATT	<u>903</u>
PMCA_00003	TGGGAACGGTGCCAAGCATT	<u>904</u>
PMCA_00004	GCCACCTCTGATGGACGAGCA	<u>905</u>
PMFE_00001	CGCGTCAACTGGGGAGATGAA	<u>906</u>
PMFE_00002	GCGCGCCTGTCTGTTCCAAT	<u>907</u>
PMFE_00003	GAGTCTTCTGGGTTGCAAAGGATGG	<u>908</u>



seqid	sequence (5'-3')	SEQ ID NO:
PMFE 00004	CCCCTGGATTGAGACCTGTTTCTTG	<u>909</u>
PMPEDV 00001	GCAGCATTGCTCTTTGGTGGTAATG	<u>910</u>
PMPEDV 00002	TGCTGAATGGTTTCACGCTTGTTCT	<u>911</u>
PMPEDV 00003	CCGCAAACGGGTGCCATTAT	<u>912</u>
PMPEDV 00004	TCGCCGTGAGGTCCTGTTCC	<u>913</u>
PMPTGV 00001	TCGCTCCAATTCCCGTGGTC	<u>914</u>
PMPTGV 00002	ACGTTGGCCCTTCACCATGC	<u>915</u>
PMPTGV 00003	CAAGCATTACCCACAATTGGCTGAA	<u>916</u>
PMPTGV 00004	TTCTTTTGCCACTTCTGATGGACGA	<u>917</u>
PMBOV 00001	TTCCTTTAAACAGCCGATGGCAAC	<u>918</u>
PMBOV 00002	TCGGAATAGCCTCATCGCTACTTGG	<u>919</u>
PMBOV 00003	TTCCGCCTGGCACGGTACTC	<u>920</u>
PMBOV 00004	TGGCTTAGCGGCATCCTTGC	<u>921</u>
PMFIPV 00001	CACCATGGCCTCAGCCTTGA	<u>922</u>
PMFIPV 00002	GTGCCGCCAACCTGCCAGTA	<u>923</u>
PMFIPV 00003	GGTCTTGGCACTGTGGATGATGATT	<u>924</u>
PMFIPV 00004	GAAAAAGGGACAGCTACAGCGGATG	<u>925</u>
PMR 00001	CCCAATCAGAATTTTGAGGCTCTG	<u>926</u>
PMR 00002	AGCGAATTGCACCTGAATACTGCAA	<u>927</u>
PMR 00003	TGACCAAACCGAGCGTGCAG	<u>928</u>
PMR 00004	CAGTGGCGGGGATTCCATTG	<u>929</u>
PMPHEV 00001	AGCGTCAACTGCTGCCACGA	<u>930</u>
PMPHEV 00002	AGTACCGTGCCAGGCGGAAA	<u>931</u>
PMPHEV 00003	AAGGTGTGCCTATTGCACCAGGAGT	<u>932</u>
PMPHEV 00004	ACTAGCGACCCAGAAGACTCCGTCA	<u>933</u>
PMPV 00001	AGAAGACCACTTGGGCTGACCAAAC	<u>934</u>
PMPV 00002	TTGGCAATAGGCACTCCTTGTCTT	<u>935</u>
PMPV 00003	GCGCCAGCCTGCCTCTATTG	<u>936</u>
PMPV 00004	TGGGGCCCCCTCTTTCCAAAA	<u>937</u>

seqid	sequence (5'-3')	<u>SEQ ID NO:</u>
PMTK 00001	ATGGCTCACC GCCGTATTG	<u>938</u>
PMTK 00002	TGGGCGTCACTCTGCTTCCA	<u>939</u>
PMTK 00003	GCTAAGGCTGATGAAATGGCTCACC	<u>940</u>
PMTK 00004	TCCAAAAAGACAAGCATGGCTGCTA	<u>941</u>
PMSDAV 00001	TCTATGTTGAAGGCTCGGGAAGGTC	<u>942</u>
PMSDAV 00002	TACTTGCTTAGGCTGTCCGGCATCT	<u>943</u>
PMSDAV 00003	AGCAGTGCCCAGTGCAGCAG	<u>944</u>
PMSDAV 00004	TGGGTT CATCAACGCCACCA	<u>945</u>